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(54) Title: NOVEL COMPOUNDS

(57) Abstract: Polypeptides and polynucleotides of the genes set forth in Table I and methods for producing such polypeptides by recombinant techniques are disclosed. Also disclosed are methods for utilizing polypeptides and polynucleotides of the genes set forth in Table I in diagnostic assays.

Novel Compounds

Field of Invention

This invention relates to newly identified polypeptides and polynucleotides encoding such polypeptides, to their use in diagnosis and in identifying compounds that may be agonists, antagonists that are potentially useful in therapy, and to production of such polypeptides and polynucleotides. The polynucleotides and polypeptides of the present invention also relate to proteins with signal sequences which allow them to be secreted extracellularly or membrane-associated (hereinafter often referred collectively as secreted proteins or secreted polypeptides).

Background of the Invention

The drug discovery process is currently undergoing a fundamental revolution as it embraces "functional genomics", that is, high throughput genome- or gene-based biology. This approach as a means to identify genes and gene products as therapeutic targets is rapidly superseding earlier approaches based on "positional cloning". A phenotype, that is a biological function or genetic disease, would be identified and this would then be tracked back to the responsible gene, based on its genetic map position.

Functional genomics relies heavily on high-throughput DNA sequencing technologies and the various tools of bioinformatics to identify gene sequences of potential interest from the many molecular biology databases now available. There is a continuing need to identify and characterise further genes and their related polypeptides/proteins, as targets for drug discovery.

Proteins and polypeptides that are naturally secreted into blood, lymph and other body fluids, or secreted into the cellular membrane are of primary interest for pharmaceutical research and development. The reason for this interest is the relative ease to target protein therapeutics into their place of action (body fluids or the cellular membrane). The natural pathway for protein secretion into extracellular space is the endoplasmic reticulum in eukaryotes and the inner membrane in prokaryotes (Palade, 1975, *Science*, 189, 347; Milstein, Brownlee, Harrison, and Mathews, 1972, *Nature New Biol.*, 239, 117; Blobel, and Dobberstein, 1975, *J. Cell. Biol.*, 67, 835). On the other hand, there is no known natural pathway for exporting a protein from the exterior of the cells into the cytosol (with the exception of pinocytosis, a mechanism of snake venom toxin intrusion into cells). Therefore targeting protein therapeutics into cells poses extreme difficulties.

The secreted and membrane-associated proteins include but are not limited to all peptide hormones and their receptors (including but not limited to insulin, growth hormones, chemokines, cytokines, neuropeptides, integrins, kallikreins, lamins, melanins, natriuretic hormones, neropsin, neurotropins, pituitary hormones, pleiotropins, prostaglandins, secretogranins, selectins, thromboglobulins, thymosins), the breast and colon cancer gene products, leptin, the obesity gene protein and its receptors, serum albumin, superoxide dismutase, spliceosome proteins, 7TM (transmembrane) proteins also called as G-protein coupled receptors, immunoglobulins, several families of serine proteinases (including but not limited to proteins of the blood coagulation cascade, digestive enzymes), deoxyribonuclease I, etc.

Therapeutics based on secreted or membrane-associated proteins approved by FDA or foreign agencies include but are not limited to insulin, glucagon, growth hormone, chorionic gonadotropin, follicle stimulating hormone, luteinizing hormone, calcitonin, adrenocorticotrophic hormone (ACTH), vasopressin, interleukines, interferones, immunoglobulins, lactoferrin (diverse products marketed by several companies), tissue-type plasminogen activator (Alteplase by Genentech), hyaularindase (Wydase by Wyeth-Ayerst), dornase alpha (Pulmozyme by Genentech), Chymodictin (chymopapain by Knoll), alglucerase (Ceredase by Genzyme), streptokinase (Kabikinase by Pharmacia) (Streptase by Astra), etc. This indicates that secreted and membrane-associated proteins have an established, proven history as therapeutic targets. Clearly, there is a need for identification and characterization of further secreted and membrane-associated proteins which can play a role in preventing, ameliorating or correcting dysfunction or disease, including but not limited to diabetes, breast-, prostate-, colon cancer and other malignant tumors, hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities, asthma, manic depression, dementia, delirium, mental retardation, Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental or sexual development disorders, and dysfunctions of the blood cascade system including those leading to stroke. The proteins of the present invention which include the signal sequences are also useful to further elucidate the mechanism of protein transport which at present is not entirely understood, and thus can be used as research tools.

Summary of the Invention

The present invention relates to particular polypeptides and polynucleotides of the genes set forth in Table I, including recombinant materials and methods for their production. Such polypeptides and polynucleotides are of interest in relation to methods of treatment of certain diseases, including, but not limited to, the diseases set forth in Tables III and V, 5 hereinafter referred to as "diseases of the invention". In a further aspect, the invention relates to methods for identifying agonists and antagonists (e.g., inhibitors) using the materials provided by the invention, and treating conditions associated with imbalance of polypeptides and/or polynucleotides of the genes set forth in Table I with the identified compounds. In still a further aspect, the invention relates to diagnostic assays for detecting 10 diseases associated with inappropriate activity or levels the genes set forth in Table I. Another aspect of the invention concerns a polynucleotide comprising any of the nucleotide sequences set forth in the Sequence Listing and a polypeptide comprising a polypeptide encoded by the nucleotide sequence. In another aspect, the invention relates to a polypeptide comprising any of the polypeptide sequences set forth in the Sequence Listing and 15 recombinant materials and methods for their production. Another aspect of the invention relates to methods for using such polypeptides and polynucleotides. Such uses include the treatment of diseases, abnormalities and disorders (hereinafter simply referred to as diseases) caused by abnormal expression, production, function and or metabolism of the genes of this invention, and such diseases are readily apparent by those skilled in the art from the homology 20 to other proteins disclosed for each attached sequence. In still another aspect, the invention relates to methods to identify agonists and antagonists using the materials provided by the invention, and treating conditions associated with the imbalance with the identified compounds. Yet another aspect of the invention relates to diagnostic assays for detecting 25 diseases associated with inappropriate activity or levels of the secreted proteins of the present invention.

Description of the Invention

In a first aspect, the present invention relates to polypeptides the genes set forth in Table I. Such polypeptides include:

30 (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in the Sequence Listing, herein when referring to polynucleotides or polypeptides of the Sequence Listing, a reference is also made to the Sequence Listing referred to in the Sequence Listing;

(b) an isolated polypeptide comprising a polypeptide sequence having at least 95%, 96%, 35 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;

(c) an isolated polypeptide comprising a polypeptide sequence set forth in the Sequence Listing;

(d) an isolated polypeptide having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;

5 (e) a polypeptide sequence set forth in the Sequence Listing; and

(f) an isolated polypeptide having or comprising a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing;

(g) fragments and variants of such polypeptides in (a) to (f).

10 Polypeptides of the present invention are believed to be members of the gene families set forth in Table II. They are therefore of therapeutic and diagnostic interest for the reasons set forth in Tables III and V. The biological properties of the polypeptides and polynucleotides of the genes set forth in Table I are hereinafter referred to as "the biological activity" of polypeptides and polynucleotides of the genes set forth in Table I. Preferably, a

15 polypeptide of the present invention exhibits at least one biological activity of the genes set forth in Table I.

Polypeptides of the present invention also include variants of the aforementioned polypeptides, including all allelic forms and splice variants. Such polypeptides vary from the reference polypeptide by insertions, deletions, and substitutions that may be

20 conservative or non-conservative, or any combination thereof. Particularly preferred variants are those in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acids are inserted, substituted, or deleted, in any combination.

Preferred fragments of polypeptides of the present invention include an isolated

25 polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids from an amino acid sequence set forth in the Sequence Listing, or an isolated polypeptide comprising an amino acid sequence having at least 30, 50 or 100 contiguous amino acids truncated or deleted from an amino acid sequence set forth in the Sequence Listing. Preferred fragments are biologically active fragments that mediate the biological

30 activity of polypeptides and polynucleotides of the genes set forth in Table I, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Also preferred are those fragments that are antigenic or immunogenic in an animal, especially in a human.

Fragments of a polypeptide of the invention may be employed for producing the

35 corresponding full-length polypeptide by peptide synthesis; therefore, these variants may be

employed as intermediates for producing the full-length polypeptides of the invention. A polypeptide of the present invention may be in the form of the "mature" protein or may be a part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence that contains secretory or leader sequences, pro-
5 sequences, sequences that aid in purification, for instance multiple histidine residues, or an additional sequence for stability during recombinant production.

Polypeptides of the present invention can be prepared in any suitable manner, for instance by isolation from naturally occurring sources, from genetically engineered host cells comprising expression systems (*vide infra*) or by chemical synthesis, using for instance
10 automated peptide synthesizers, or a combination of such methods. Means for preparing such polypeptides are well understood in the art.

In a further aspect, the present invention relates to polynucleotides of the genes set forth in Table I. Such polynucleotides include:

- (a) an isolated polynucleotide comprising a polynucleotide sequence having at least 95%,
15 96%, 97%, 98%, or 99% identity to a polynucleotide sequence set forth in the Sequence Listing;
- (b) an isolated polynucleotide comprising a polynucleotide set forth in the Sequence Listing;
- (c) an isolated polynucleotide having at least 95%, 96%, 97%, 98%, or 99% identity to a
20 polynucleotide set forth in the Sequence Listing;
- (d) an isolated polynucleotide set forth in the Sequence Listing;
- (e) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- 25 (f) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing;
- (g) an isolated polynucleotide having a polynucleotide sequence encoding a polypeptide sequence having at least 95%, 96%, 97%, 98%, or 99% identity to a polypeptide sequence set forth in the Sequence Listing;
- 30 (h) an isolated polynucleotide encoding a polypeptide set forth in the Sequence Listing;
- (i) an isolated polynucleotide having or comprising a polynucleotide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polynucleotide sequence set forth in the Sequence Listing;

(j) an isolated polynucleotide having or comprising a polynucleotide sequence encoding a polypeptide sequence that has an Identity Index of 0.95, 0.96, 0.97, 0.98, or 0.99 compared to a polypeptide sequence set forth in the Sequence Listing; and
5 polynucleotides that are fragments and variants of the above mentioned polynucleotides or that are complementary to above mentioned polynucleotides, over the entire length thereof.

Preferred fragments of polynucleotides of the present invention include an isolated polynucleotide comprising an nucleotide sequence having at least 15, 30, 50 or 100 contiguous nucleotides from a sequence set forth in the Sequence Listing, or an isolated polynucleotide comprising a sequence having at least 30, 50 or 100 contiguous nucleotides 10 truncated or deleted from a sequence set forth in the Sequence Listing.

Preferred variants of polynucleotides of the present invention include splice variants, allelic variants, and polymorphisms, including polynucleotides having one or more single nucleotide polymorphisms (SNPs).

Polynucleotides of the present invention also include polynucleotides encoding 15 polypeptide variants that comprise an amino acid sequence set forth in the Sequence Listing and in which several, for instance from 50 to 30, from 30 to 20, from 20 to 10, from 10 to 5, from 5 to 3, from 3 to 2, from 2 to 1 or 1 amino acid residues are substituted, deleted or added, in any combination.

In a further aspect, the present invention provides polynucleotides that are RNA transcripts 20 of the DNA sequences of the present invention. Accordingly, there is provided an RNA polynucleotide that:

- (a) comprises an RNA transcript of the DNA sequence encoding a polypeptide set forth in the Sequence Listing;
- (b) is a RNA transcript of a DNA sequence encoding a polypeptide set forth in the 25 Sequence Listing;
- (c) comprises an RNA transcript of a DNA sequence set forth in the Sequence Listing; or
- (d) is a RNA transcript of a DNA sequence set forth in the Sequence Listing;

and RNA polynucleotides that are complementary thereto.

30 The polynucleotide sequences set forth in the Sequence Listing show homology with the polynucleotide sequences set forth in Table II. A polynucleotide sequence set forth in the Sequence Listing is a cDNA sequence that encodes a polypeptide set forth in the Sequence Listing. A polynucleotide sequence encoding a polypeptide set forth in the Sequence Listing may be identical to a polypeptide encoding a sequence set forth in the 35 Sequence Listing or it may be a sequence other than a sequence set forth in the Sequence

Listing, which, as a result of the redundancy (degeneracy) of the genetic code, also encodes a polypeptide set forth in the Sequence Listing. A polypeptide of a sequence set forth in the Sequence Listing is related to other proteins of the gene families set forth in Table II, having homology and/or structural similarity with the polypeptides set forth in Table II. Preferred 5 polypeptides and polynucleotides of the present invention are expected to have, *inter alia*, similar biological functions/properties to their homologous polypeptides and polynucleotides. Furthermore, preferred polypeptides and polynucleotides of the present invention have at least one activity of the genes set forth in Table I.

Polynucleotides of the present invention may be obtained using standard cloning 10 and screening techniques from a cDNA library derived from mRNA from the tissues set forth in Table IV (see for instance, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)). Polynucleotides of the invention can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available 15 techniques.

When polynucleotides of the present invention are used for the recombinant production of polypeptides of the present invention, the polynucleotide may include the 20 coding sequence for the mature polypeptide, by itself, or the coding sequence for the mature polypeptide in reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, or pro- or prepro- protein sequence, or other fusion peptide portions. For example, a marker sequence that facilitates purification of the fused 25 polypeptide can be encoded. In certain preferred embodiments of this aspect of the invention, the marker sequence is a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al.*, Proc Natl Acad Sci USA (1989) 86:821-824, or is an HA tag. A polynucleotide may also contain non-coding 5' and 3' sequences, such as 30 transcribed, non-translated sequences, splicing and polyadenylation signals, ribosome binding sites and sequences that stabilize mRNA.

Polynucleotides that are identical, or have sufficient identity to a polynucleotide 35 sequence set forth in the Sequence Listing, may be used as hybridization probes for cDNA and genomic DNA or as primers for a nucleic acid amplification reaction (for instance, PCR). Such probes and primers may be used to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes (including genes encoding paralogs from human sources and orthologs and paralogs from other species) that have a high sequence similarity to sequences set forth in the Sequence Listing, typically at least 95% identity. Preferred probes and primers will

generally comprise at least 15 nucleotides, preferably, at least 30 nucleotides and may have at least 50, if not at least 100 nucleotides. Particularly preferred probes will have between 30 and 50 nucleotides. Particularly preferred primers will have between 20 and 25 nucleotides.

5 A polynucleotide encoding a polypeptide of the present invention, including homologs from other species, may be obtained by a process comprising the steps of screening a library under stringent hybridization conditions with a labeled probe having a sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides; and isolating full-length cDNA and genomic clones containing the

10 polynucleotide sequence set forth in the Sequence Listing. Such hybridization techniques are well known to the skilled artisan. Preferred stringent hybridization conditions include overnight incubation at 42°C in a solution comprising: 50% formamide, 5xSSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10 % dextran sulfate, and 20 microgram/ml denatured, sheared salmon sperm DNA;

15 followed by washing the filters in 0.1x SSC at about 65°C. Thus the present invention also includes isolated polynucleotides, preferably with a nucleotide sequence of at least 100, obtained by screening a library under stringent hybridization conditions with a labeled probe having the sequence set forth in the Sequence Listing or a fragment thereof, preferably of at least 15 nucleotides.

20 The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide does not extend all the way through to the 5' terminus. This is a consequence of reverse transcriptase, an enzyme with inherently low "processivity" (a measure of the ability of the enzyme to remain attached to the template during the polymerisation reaction), failing to complete a DNA copy of the mRNA template during first strand cDNA synthesis.

25 There are several methods available and well known to those skilled in the art to obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA ends (RACE) (see, for example, Frohman et al., Proc Nat Acad Sci USA 85, 8998-9002, 1988). Recent modifications of the technique, exemplified

30 by the Marathon (trade mark) technology (Clontech Laboratories Inc.) for example, have significantly simplified the search for longer cDNAs. In the Marathon (trade mark) technology, cDNAs have been prepared from mRNA extracted from a chosen tissue and an 'adaptor' sequence ligated onto each end. Nucleic acid amplification (PCR) is then carried out to amplify the "missing" 5' end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using 'nested'

primers, that is, primers designed to anneal within the amplified product (typically an adapter specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the known gene sequence). The products of this reaction can then be analyzed by DNA sequencing and a full-length cDNA constructed either by 5 joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full-length PCR using the new sequence information for the design of the 5' primer.

Recombinant polypeptides of the present invention may be prepared by processes well known in the art from genetically engineered host cells comprising expression systems. 10 Accordingly, in a further aspect, the present invention relates to expression systems comprising a polynucleotide or polynucleotides of the present invention, to host cells which are genetically engineered with such expression systems and to the production of polypeptides of the invention by recombinant techniques. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of 15 the present invention.

For recombinant production, host cells can be genetically engineered to incorporate expression systems or portions thereof for polynucleotides of the present invention.

Polynucleotides may be introduced into host cells by methods described in many standard laboratory manuals, such as Davis et al., *Basic Methods in Molecular Biology* (1986) and 20 Sambrook et al. (*ibid*). Preferred methods of introducing polynucleotides into host cells include, for instance, calcium phosphate transfection, DEAE-dextran mediated transfection, transvection, micro-injection, cationic lipid-mediated transfection, electroporation, transduction, scrape loading, ballistic introduction or infection.

Representative examples of appropriate hosts include bacterial cells, such as 25 *Streptococci*, *Staphylococci*, *E. coli*, *Streptomyces* and *Bacillus subtilis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as *Drosophila S2* and *Spodoptera Sf9* cells; animal cells such as CHO, COS, HeLa, C127, 3T3, BHK, HEK 293 and Bowes melanoma cells; and plant cells.

A great variety of expression systems can be used, for instance, chromosomal, 30 episomal and virus-derived systems, e.g., vectors derived from bacterial plasmids, from bacteriophage, from transposons, from yeast episomes, from insertion elements, from yeast chromosomal elements, from viruses such as baculoviruses, papova viruses, such as SV40, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as those derived from plasmid and 35 bacteriophage genetic elements, such as cosmids and phagemids. The expression systems

may contain control regions that regulate as well as engender expression. Generally, any system or vector that is able to maintain, propagate or express a polynucleotide to produce a polypeptide in a host may be used. The appropriate polynucleotide sequence may be inserted into an expression system by any of a variety of well-known and routine techniques, such as, for example, those set forth in Sambrook *et al.*, (*ibid*). Appropriate secretion signals may be incorporated into the desired polypeptide to allow secretion of the translated protein into the lumen of the endoplasmic reticulum, the periplasmic space or the extracellular environment. These signals may be endogenous to the polypeptide or they may be heterologous signals.

If a polypeptide of the present invention is to be expressed for use in screening assays, it is generally preferred that the polypeptide be produced at the surface of the cell. In this event, the cells may be harvested prior to use in the screening assay. If the polypeptide is secreted into the medium, the medium can be recovered in order to recover and purify the polypeptide. If produced intracellularly, the cells must first be lysed before the polypeptide is recovered.

Polypeptides of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation and/or purification.

Polynucleotides of the present invention may be used as diagnostic reagents, through detecting mutations in the associated gene. Detection of a mutated form of a gene is characterized by the polynucleotides set forth in the Sequence Listing in the cDNA or genomic sequence and which is associated with a dysfunction. Will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered spatial or temporal expression of the gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques well known in the art.

Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or it may be amplified enzymatically by using PCR, preferably RT-PCR, or other amplification techniques prior to analysis. RNA or cDNA may also be used

in similar fashion. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to labeled nucleotide sequences of the genes set forth in Table I. Perfectly matched sequences can be distinguished from mismatched duplexes by 5 RNase digestion or by differences in melting temperatures. DNA sequence difference may also be detected by alterations in the electrophoretic mobility of DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing (see, for instance, Myers *et al.*, *Science* (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as RNase and S1 protection or the chemical cleavage 10 method (see Cotton *et al.*, *Proc Natl Acad Sci USA* (1985) 85: 4397-4401).

An array of oligonucleotides probes comprising polynucleotide sequences or fragments thereof of the genes set forth in Table I can be constructed to conduct efficient screening of *e.g.*, genetic mutations. Such arrays are preferably high density arrays or grids. Array technology methods are well known and have general applicability and can be used to 15 address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability, see, for example, M. Chee *et al.*, *Science*, 274, 610-613 (1996) and other references cited therein.

Detection of abnormally decreased or increased levels of polypeptide or mRNA expression may also be used for diagnosing or determining susceptibility of a subject to a disease of the 20 invention. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample 25 derived from a host are well-known to those of skill in the art. Such assay methods include radio-immunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagnostic kit comprising:
(a) a polynucleotide of the present invention, preferably the nucleotide sequence set forth in the Sequence Listing, or a fragment or an RNA transcript thereof;
30 (b) a nucleotide sequence complementary to that of (a);
(c) a polypeptide of the present invention, preferably the polypeptide set forth in the Sequence Listing or a fragment thereof; or
(d) an antibody to a polypeptide of the present invention, preferably to the polypeptide set forth in the Sequence Listing.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing a disease or susceptibility to a disease, particularly diseases of the invention, amongst others.

The polynucleotide sequences of the present invention are valuable for chromosome localisation studies. The sequences set forth in the Sequence Listing are specifically targeted to, and can hybridize with, a particular location on an individual human chromosome. The mapping of relevant sequences to chromosomes according to the present invention is an important first step in correlating those sequences with gene associated disease. Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such data are found in, for example, V. McKusick, Mendelian Inheritance in Man (available online through Johns Hopkins University Welch Medical Library). The relationship between genes and diseases that have been mapped to the same chromosomal region are then identified through linkage analysis (co-inheritance of physically adjacent genes). Precise human chromosomal localisations for a genomic sequence (gene fragment etc.) can be determined using Radiation Hybrid (RH) Mapping (Walter, M. Spillett, D., Thomas, P., Weissenbach, J., and Goodfellow, P., (1994) A method for constructing radiation hybrid maps of whole genomes, *Nature Genetics* 7, 22-28). A number of RH panels are available from Research Genetics (Huntsville, AL, USA) e.g. the GeneBridge4 RH panel (Hum Mol Genet 1996 Mar;5(3):339-46 A radiation hybrid map of the human genome. Gyapay G, Schmitt K, Fizames C, Jones H, Vega-Czarny N, Spillett D, Muselet D, Prud'Homme JF, Dib C, Auffray C, Morissette J, Weissenbach J, Goodfellow PN). To determine the chromosomal location of a gene using this panel, 93 PCRs are performed using primers designed from the gene of interest on RH DNAs. Each of these DNAs contains random human genomic fragments maintained in a hamster background (human / hamster hybrid cell lines). These PCRs result in 93 scores indicating the presence or absence of the PCR product of the gene of interest. These scores are compared with scores created using PCR products from genomic sequences of known location. This comparison is conducted at <http://www.genome.wi.mit.edu/>.

The polynucleotide sequences of the present invention are also valuable tools for tissue expression studies. Such studies allow the determination of expression patterns of polynucleotides of the present invention which may give an indication as to the expression patterns of the encoded polypeptides in tissues, by detecting the mRNAs that encode them. The techniques used are well known in the art and include *in situ* hybridization techniques to clones arrayed on a grid, such as cDNA microarray hybridization (Schena *et al*, *Science*,

270, 467-470, 1995 and Shalon *et al.*, *Genome Res.*, 6, 639-645, 1996) and nucleotide amplification techniques such as PCR. A preferred method uses the TAQMAN (Trade mark) technology available from Perkin Elmer. Results from these studies can provide an indication of the normal function of the polypeptide in the organism. In addition, 5 comparative studies of the normal expression pattern of mRNAs with that of mRNAs encoded by an alternative form of the same gene (for example, one having an alteration in polypeptide coding potential or a regulatory mutation) can provide valuable insights into the role of the polypeptides of the present invention, or that of inappropriate expression thereof in disease. Such inappropriate expression may be of a temporal, spatial or simply 10 quantitative nature.

A further aspect of the present invention relates to antibodies. The polypeptides of the invention or their fragments, or cells expressing them, can be used as immunogens to produce antibodies that are immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the 15 polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against polypeptides of the present invention may be obtained by administering the polypeptides or epitope-bearing fragments, or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal 20 antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler, G. and Milstein, C., *Nature* (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, 77-96, Alan R. Liss, 25 Inc., 1985).

Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

30 The above-described antibodies may be employed to isolate or to identify clones expressing the polypeptide or to purify the polypeptides by affinity chromatography. Antibodies against polypeptides of the present invention may also be employed to treat diseases of the invention, amongst others.

35 Polypeptides and polynucleotides of the present invention may also be used as vaccines. Accordingly, in a further aspect, the present invention relates to a method for

inducing an immunological response in a mammal that comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response, including, for example, cytokine-producing T cells or cytotoxic T cells, to protect said animal from disease, whether that disease is already established within the
5 individual or not. An immunological response in a mammal may also be induced by a method comprises delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce such an immunological response to produce antibody to protect said animal from diseases of the invention. One way of administering the vector is by accelerating it into the desired
10 cells as a coating on particles or otherwise. Such nucleic acid vector may comprise DNA, RNA, a modified nucleic acid, or a DNA/RNA hybrid. For use a vaccine, a polypeptide or a nucleic acid vector will be normally provided as a vaccine formulation (composition). The formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered parenterally (for instance, subcutaneous,
15 intra-muscular, intravenous, or intra-dermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions that may contain anti-oxidants, buffers, bacteriostats and solutes that render the formulation isotonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions that may include suspending agents or thickening agents. The formulations may be presented in unit-dose or
20 multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily
25 determined by routine experimentation.

Polypeptides of the present invention have one or more biological functions that are of relevance in one or more disease states, in particular the diseases of the invention hereinbefore mentioned. It is therefore useful to identify compounds that stimulate or inhibit the function or level of the polypeptide. Accordingly, in a further aspect, the present
30 invention provides for a method of screening compounds to identify those that stimulate or inhibit the function or level of the polypeptide. Such methods identify agonists or antagonists that may be employed for therapeutic and prophylactic purposes for such diseases of the invention as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, collections
35 of chemical compounds, and natural product mixtures. Such agonists or antagonists so-

identified may be natural or modified substrates, ligands, receptors, enzymes, etc., as the case may be, of the polypeptide; a structural or functional mimetic thereof (see Coligan *et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)) or a small molecule. Such small molecules preferably have a molecular weight below 2,000 daltons, more preferably 5 between 300 and 1,000 daltons, and most preferably between 400 and 700 daltons. It is preferred that these small molecules are organic molecules.

The screening method may simply measure the binding of a candidate compound to the polypeptide, or to cells or membranes bearing the polypeptide, or a fusion protein thereof, by means of a label directly or indirectly associated with the candidate compound. 10 Alternatively, the screening method may involve measuring or detecting (qualitatively or quantitatively) the competitive binding of a candidate compound to the polypeptide against a labeled competitor (*e.g.* agonist or antagonist). Further, these screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the cells bearing the polypeptide. 15 Inhibitors of activation are generally assayed in the presence of a known agonist and the effect on activation by the agonist by the presence of the candidate compound is observed. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide of the present invention, to form a mixture, measuring an activity of the genes set forth in Table I in the mixture, and 20 comparing activity of the mixture of the genes set forth in Table I to a control mixture which contains no candidate compound.

Polypeptides of the present invention may be employed in conventional low capacity screening methods and also in high-throughput screening (HTS) formats. Such HTS formats include not only the well-established use of 96- and, more recently, 384-well 25 micotiter plates but also emerging methods such as the nanowell method described by Schullek *et al.*, Anal Biochem., 246, 20-29, (1997). Fusion proteins, such as those made from Fc portion and polypeptide of the genes set forth in Table I, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, J 30 Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, J Biol Chem, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the polypeptide of the present invention may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA 35 assay may be constructed for measuring secreted or cell associated levels of polypeptide

using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents that may inhibit or enhance the production of polypeptide (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

A polypeptide of the present invention may be used to identify membrane bound or 5 soluble receptors, if any, through standard receptor binding techniques known in the art. These include, but are not limited to, ligand binding and crosslinking assays in which the polypeptide is labeled with a radioactive isotope (for instance, ^{125}I), chemically modified (for instance, biotinylated), or fused to a peptide sequence suitable for detection or 10 purification, and incubated with a source of the putative receptor (cells, cell membranes, cell supernatants, tissue extracts, bodily fluids). Other methods include biophysical techniques such as surface plasmon resonance and spectroscopy. These screening methods may also be used to identify agonists and antagonists of the polypeptide that compete with the binding of the polypeptide to its receptors, if any. Standard methods for conducting such assays are well understood in the art.

15 Examples of antagonists of polypeptides of the present invention include antibodies or, in some cases, oligonucleotides or proteins that are closely related to the ligands, substrates, receptors, enzymes, etc., as the case may be, of the polypeptide, *e.g.*, a fragment of the ligands, substrates, receptors, enzymes, etc.; or a small molecule that bind to the 20 polypeptide of the present invention but do not elicit a response, so that the activity of the polypeptide is prevented.

Screening methods may also involve the use of transgenic technology and the genes set forth in Table I. The art of constructing transgenic animals is well established. For example, the genes set forth in Table I may be introduced through microinjection into the male pronucleus of fertilized oocytes, retroviral transfer into pre- or post-implantation 25 embryos, or injection of genetically modified, such as by electroporation, embryonic stem cells into host blastocysts. Particularly useful transgenic animals are so-called "knock-in" animals in which an animal gene is replaced by the human equivalent within the genome of that animal. Knock-in transgenic animals are useful in the drug discovery process, for target validation, where the compound is specific for the human target. Other useful transgenic 30 animals are so-called "knock-out" animals in which the expression of the animal ortholog of a polypeptide of the present invention and encoded by an endogenous DNA sequence in a cell is partially or completely annulled. The gene knock-out may be targeted to specific cells or tissues, may occur only in certain cells or tissues as a consequence of the limitations of the technology, or may occur in all, or substantially all, cells in the animal. Transgenic 35 animal technology also offers a whole animal expression-cloning system in which

introduced genes are expressed to give large amounts of polypeptides of the present invention

Screening kits for use in the above described methods form a further aspect of the present invention. Such screening kits comprise:

- 5 (a) a polypeptide of the present invention;
- (b) a recombinant cell expressing a polypeptide of the present invention;
- (c) a cell membrane expressing a polypeptide of the present invention; or
- (d) an antibody to a polypeptide of the present invention;

which polypeptide is preferably that set forth in the Sequence Listing.

- 10 It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

Glossary

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

"Antibodies" as used herein includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, including the products of an

Fab or other immunoglobulin expression library.

- 20 "Isolated" means altered "by the hand of man" from its natural state, *i.e.*, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. Moreover, a
- 25 polynucleotide or polypeptide that is introduced into an organism by transformation, genetic manipulation or by any other recombinant method is "isolated" even if it is still present in said organism, which organism may be living or non-living.

- 30 "Secreted protein activity or secreted polypeptide activity" or "biological activity of the secreted protein or secreted polypeptide" refers to the metabolic or physiologic function of said secreted protein including similar activities or improved activities or these activities with decreased undesirable side-effects. Also included are antigenic and immunogenic activities of said secreted protein.

"Secreted protein gene" refers to a polynucleotide comprising any of the attached nucleotide sequences or allelic variants thereof and/or their complements.

"Polynucleotide" generally refers to any polyribonucleotide (RNA) or polydeoxribonucleotide (DNA), which may be unmodified or modified RNA or DNA. "Polynucleotides" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and

5 RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, "polynucleotide" refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term "polynucleotide" also includes DNAs or RNAs containing one or more modified bases and

10 DNAs or RNAs with backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells.

15 "Polynucleotide" also embraces relatively short polynucleotides, often referred to as oligonucleotides.

"Polypeptide" refers to any polypeptide comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. "Polypeptide" refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins. Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. "Polypeptides" include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques that are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-

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linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristylation, oxidation, proteolytic processing, phosphorylation, prenylation,
5 racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, Proteins - Structure and Molecular Properties, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., Post-translational Protein Modifications: Perspectives and Prospects, 1-12, in Post-translational Covalent Modification of Proteins, B. C. Johnson, Ed., Academic Press, 10 New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", Meth Enzymol, 182, 626-646, 1990, and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", Ann NY Acad Sci, 663, 48-62, 1992).

"Fragment" of a polypeptide sequence refers to a polypeptide sequence that is shorter than the reference sequence but that retains essentially the same biological function or activity as the reference polypeptide. "Fragment" of a polynucleotide sequence refers to a polynucleotide sequence that is shorter than the reference sequence set forth in the Sequence Listing.
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"Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains the essential properties thereof. A typical variant of a polynucleotide differs in nucleotide sequence from the reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from the reference polypeptide. Generally, alterations are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, insertions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. Typical conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe and Tyr. A variant of a polynucleotide or polypeptide may be naturally occurring such as an allele, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis. Also included as variants are polypeptides having one or more post-translational modifications, for
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instance glycosylation, phosphorylation, methylation, ADP ribosylation and the like.

Embodiments include methylation of the N-terminal amino acid, phosphorylations of serines and threonines and modification of C-terminal glycines.

5 "Allele" refers to one of two or more alternative forms of a gene occurring at a given locus in the genome.

"Polymorphism" refers to a variation in nucleotide sequence (and encoded polypeptide sequence, if relevant) at a given position in the genome within a population.

10 "Single Nucleotide Polymorphism" (SNP) refers to the occurrence of nucleotide variability at a single nucleotide position in the genome, within a population. An SNP may occur within a gene or within intergenic regions of the genome. SNPs can be assayed using Allele Specific Amplification (ASA). For the process at least 3 primers are required. A common primer is used in reverse complement to the polymorphism being assayed. This common primer can be between 50 and 1500 bps from the polymorphic base. The other two (or more) primers are identical to each other except that the final 3' base wobbles to match 15 one of the two (or more) alleles that make up the polymorphism. Two (or more) PCR reactions are then conducted on sample DNA, each using the common primer and one of the Allele Specific Primers.

20 "Splice Variant" as used herein refers to cDNA molecules produced from RNA molecules initially transcribed from the same genomic DNA sequence but which have undergone alternative RNA splicing. Alternative RNA splicing occurs when a primary RNA transcript undergoes splicing, generally for the removal of introns, which results in the production of more than one mRNA molecule each of that may encode different amino acid sequences. The term splice variant also refers to the proteins encoded by the above cDNA molecules.

25 "Identity" reflects a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, determined by comparing the sequences. In general, identity refers to an exact nucleotide to nucleotide or amino acid to amino acid correspondence of the two polynucleotide or two polypeptide sequences, respectively, over the length of the sequences being compared.

30 "% Identity" - For sequences where there is not an exact correspondence, a "% identity" may be determined. In general, the two sequences to be compared are aligned to give a maximum correlation between the sequences. This may include inserting "gaps" in either one or both sequences, to enhance the degree of alignment. A % identity may be determined over the whole length of each of the sequences being compared (so-called global alignment), that is particularly suitable for sequences of the same or very similar length, or

over shorter, defined lengths (so-called local alignment), that is more suitable for sequences of unequal length.

"Similarity" is a further, more sophisticated measure of the relationship between two polypeptide sequences. In general, "similarity" means a comparison between the amino acids of two polypeptide chains, on a residue by residue basis, taking into account not only exact correspondences between a between pairs of residues, one from each of the sequences being compared (as for identity) but also, where there is not an exact correspondence, whether, on an evolutionary basis, one residue is a likely substitute for the other. This likelihood has an associated "score" from which the "% similarity" of the two sequences can then be determined.

Methods for comparing the identity and similarity of two or more sequences are well known in the art. Thus for instance, programs available in the Wisconsin Sequence Analysis Package, version 9.1 (Devereux J et al, Nucleic Acids Res, 12, 387-395, 1984, available from Genetics Computer Group, Madison, Wisconsin, USA), for example the programs BESTFIT and GAP, may be used to determine the % identity between two polynucleotides and the % identity and the % similarity between two polypeptide sequences. BESTFIT uses the "local homology" algorithm of Smith and Waterman (J Mol Biol, 147, 195-197, 1981, Advances in Applied Mathematics, 2, 482-489, 1981) and finds the best single region of similarity between two sequences. BESTFIT is more suited to comparing two polynucleotide or two polypeptide sequences that are dissimilar in length, the program assuming that the shorter sequence represents a portion of the longer. In comparison, GAP aligns two sequences, finding a "maximum similarity", according to the algorithm of Needleman and Wunsch (J Mol Biol, 48, 443-453, 1970). GAP is more suited to comparing sequences that are approximately the same length and an alignment is expected over the entire length. Preferably, the parameters "Gap Weight" and "Length Weight" used in each program are 50 and 3, for polynucleotide sequences and 12 and 4 for polypeptide sequences, respectively. Preferably, % identities and similarities are determined when the two sequences being compared are optimally aligned.

Other programs for determining identity and/or similarity between sequences are also known in the art, for instance the BLAST family of programs (Altschul S F et al, J Mol Biol, 215, 403-410, 1990, Altschul S F et al, Nucleic Acids Res., 25:389-3402, 1997, available from the National Center for Biotechnology Information (NCBI), Bethesda, Maryland, USA and accessible through the home page of the NCBI at www.ncbi.nlm.nih.gov) and FASTA (Pearson W R, Methods in Enzymology, 183, 63-99,

1990; Pearson W R and Lipman D J, Proc Nat Acad Sci USA, 85, 2444-2448, 1988,
available as part of the Wisconsin Sequence Analysis Package).

Preferably, the BLOSUM62 amino acid substitution matrix (Henikoff S and
Henikoff J G, Proc. Nat. Acad Sci. USA, 89, 10915-10919, 1992) is used in polypeptide
5 sequence comparisons including where nucleotide sequences are first translated into amino
acid sequences before comparison.

Preferably, the program BESTFIT is used to determine the % identity of a query
polynucleotide or a polypeptide sequence with respect to a reference polynucleotide or a
polypeptide sequence, the query and the reference sequence being optimally aligned and the
10 parameters of the program set at the default value, as hereinbefore described.

"Identity Index" is a measure of sequence relatedness which may be used to
compare a candidate sequence (polynucleotide or polypeptide) and a reference sequence.
Thus, for instance, a candidate polynucleotide sequence having, for example, an Identity
Index of 0.95 compared to a reference polynucleotide sequence is identical to the reference
15 sequence except that the candidate polynucleotide sequence may include on average up to
five differences per each 100 nucleotides of the reference sequence. Such differences are
selected from the group consisting of at least one nucleotide deletion, substitution, including
transition and transversion, or insertion. These differences may occur at the 5' or 3' terminal
positions of the reference polynucleotide sequence or anywhere between these terminal
20 positions, interspersed either individually among the nucleotides in the reference sequence
or in one or more contiguous groups within the reference sequence. In other words, to
obtain a polynucleotide sequence having an Identity Index of 0.95 compared to a reference
polynucleotide sequence, an average of up to 5 in every 100 of the nucleotides of the in the
reference sequence may be deleted, substituted or inserted, or any combination thereof, as
25 hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity
Index, for instance 0.96, 0.97, 0.98 and 0.99.

Similarly, for a polypeptide, a candidate polypeptide sequence having, for example,
an Identity Index of 0.95 compared to a reference polypeptide sequence is identical to the
reference sequence except that the polypeptide sequence may include an average of up to
30 five differences per each 100 amino acids of the reference sequence. Such differences are
selected from the group consisting of at least one amino acid deletion, substitution,
including conservative and non-conservative substitution, or insertion. These differences
may occur at the amino- or carboxy-terminal positions of the reference polypeptide
sequence or anywhere between these terminal positions, interspersed either individually
35 among the amino acids in the reference sequence or in one or more contiguous groups

within the reference sequence. In other words, to obtain a polypeptide sequence having an Identity Index of 0.95 compared to a reference polypeptide sequence, an average of up to 5 in every 100 of the amino acids in the reference sequence may be deleted, substituted or inserted, or any combination thereof, as hereinbefore described. The same applies *mutatis mutandis* for other values of the Identity Index, for instance 0.96, 0.97, 0.98 and 0.99.

5 The relationship between the number of nucleotide or amino acid differences and the Identity Index may be expressed in the following equation:

$$n_a \leq x_a - (x_a \cdot I),$$

in which:

10 n_a is the number of nucleotide or amino acid differences,

x_a is the total number of nucleotides or amino acids in a sequence set forth in the Sequence Listing,

I is the Identity Index,

• is the symbol for the multiplication operator, and

15 in which any non-integer product of x_a and I is rounded down to the nearest integer prior to subtracting it from x_a .

"Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a reference sequence. Such relatedness may be quantified by determining the degree of identity and/or 20 similarity between the two sequences as hereinbefore defined. Falling within this generic term are the terms "ortholog", and "paralog". "Ortholog" refers to a polynucleotide or polypeptide that is the functional equivalent of the polynucleotide or polypeptide in another species. "Paralog" refers to a polynucleotide or polypeptide that within the same species which is functionally similar.

25 "Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 533-A discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for 30 example, improved pharmacokinetic properties [see, e.g., EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified.

All publications and references, including but not limited to patents and patent applications, cited in this specification are herein incorporated by reference in their entirety 35 as if each individual publication or reference were specifically and individually indicated to

be incorporated by reference herein as being fully set forth. Any patent application to which this application claims priority is also incorporated by reference herein in its entirety in the manner described above for publications and references.

Table I.

Gene Name	GSK Gene ID	Nucleic Acid SEQ ID NO's	Corresponding Protein SEQ ID NO's
sbg318680DNase	318680	SEQ ID NO:1	SEQ ID NO:40
sbg237038SA	237038	SEQ ID NO:2 SEQ ID NO:3	SEQ ID NO:41 SEQ ID NO:42
sbg340871GPV	340871	SEQ ID NO:4	SEQ ID NO:43
sbg293416HNKS	293416	SEQ ID NO:5 SEQ ID NO:6	SEQ ID NO:44 SEQ ID NO:45
sbg257418ZP	257418	SEQ ID NO:7	SEQ ID NO:46
sbg319185CDa	319185	SEQ ID NO:8 SEQ ID NO:9	SEQ ID NO:47 SEQ ID NO:48
sbg323307KIAAa	323307	SEQ ID NO:10	SEQ ID NO:49
sbg315953GPPa	315953	SEQ ID NO:11 SEQ ID NO:12	SEQ ID NO:50 SEQ ID NO:51
sbg318486ONC	318486	SEQ ID NO:13	SEQ ID NO:52
sbg299359LIPO	299359	SEQ ID NO:14	SEQ ID NO:53
sbg230022NGa	230022	SEQ ID NO:15 SEQ ID NO:16	SEQ ID NO:54 SEQ ID NO:55
sbg297169BGP	297169	SEQ ID NO:17 SEQ ID NO:18	SEQ ID NO:56 SEQ ID NO:57

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sbg253919HSCCAa	253919	SEQ ID NO:19 SEQ ID NO:20	SEQ ID NO:58 SEQ ID NO:59
sbg228137OLF	228137	SEQ ID NO:21 SEQ ID NO:22	SEQ ID NO:60 SEQ ID NO:61
sbg378514Netrin	378514	SEQ ID NO:23 SEQ ID NO:24	SEQ ID NO:62 SEQ ID NO:63
sbg253227.mucous matrix glycoprotein	253227	SEQ ID NO:25 SEQ ID NO:26	SEQ ID NO:64 SEQ ID NO:65
sbg262831SIAa	262831	SEQ ID NO:27 SEQ ID NO:28	SEQ ID NO:66 SEQ ID NO:67
sbg233728LIPASE	233728	SEQ ID NO:29	SEQ ID NO:68
sbg400455.CRF	400455	SEQ ID NO:30	SEQ ID NO:69
sbg400612KINASEa	400612	SEQ ID NO:31	SEQ ID NO:70
sbg381373ACRP	381373	SEQ ID NO:32	SEQ ID NO:71
sbg401294MEX-3	401294	SEQ ID NO:33 SEQ ID NO:34	SEQ ID NO:72 SEQ ID NO:73
sbg247722Cadherin	247722	SEQ ID NO:35 SEQ ID NO:36	SEQ ID NO:74 SEQ ID NO:75
sbg391057THIPa	391057	SEQ ID NO:37 SEQ ID NO:38	SEQ ID NO:76 SEQ ID NO:77
sbg378067TGFc	378067	SEQ ID NO:39	SEQ ID NO:78

Table II

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg318680-DNase	DNase I	GB:AC022471 Submitted (04-FEB-2000) by Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA.	Human DNase I-like endonuclease, gi:5803007 Parrish JE, Ciccodicola A, Wehhert M, Cox GF, Chen E, and Nelson DL; 1995; Hum. Mol. Genet. 4:1557-1564.	Secreted
sbg237038-SA	SA protein	GB:AC023292 Submitted (11-FEB-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Human SA gene, gi:2988399 Loftus,B.J. et al. Genomics 60 (3), 295- 308 (1999)	Secreted
sbg340871-GPV	Platelet glycoprotein (GPV)	GB:AC025389 Submitted (08-MAR-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Rat platelet glycoprotein V (GPV) precursor, gi:6980974 Ravanat C, Morales M, Azorsa DO, Moog S, Schuhler S, Grunert P, Loew D, Van Dorsselaer A, Cazenave JP, Lanza F; 1997; Blood 89:3253-62.	Secreted
sbg293416-HNKS	HNK-1 sulfotransfere se	JGI:LLNL-R_241B6 Joint Genome Institute, Department of Energy, USA	Human GalNAc 4- sulfotransferase, gi:11990885 Okuda,T., Mita,S., Yamauchi,S., Fukuta,M., Nakano,H., Sawada,T. and Habuchi,O. J. Biol. Chem. 275 (51), 40605- 40613 (2000)	Secreted
sbg257418-ZP	Zona pellucida protein	GB:AP000777 Submitted (25-NOV-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1- 15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan.	Mouse zona pellucida glycoprotein, gi:6677653 Epifano,O., Liang,L.F., Familiari,M., Moos,M.C. Jr. and Dean,J.; 1995; Development 121:1947- 1956.	Secreted

Table II (c nt).

Gene Name	Gene Family	Closest Polynuclotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg319185-CDa	Leukocyte differentiation antigen	GB:AC024004 Submitted (20-FEB-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Human leukocyte differentiation antigen CD84 isoform CD84s, gi:6650112 Submitted (20-MAR-1998) by Servicio de Immunologia, Hospital Clinic, Villarroel 170, Barcelona 08036, Spain	Secreted
sbg32330 7-KIAAa	Slit-like	GB:AL160156, Submitted (10-MAR-2000) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human unnamed protein, gi:10439289 Submitted (29-AUG-2000) by Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan	Secreted
sbg31595 3-GPPa	Granulocyte peptide A	GB:AC011666 Submitted (09-OCT-1999) by Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA	Human hypothetical protein SBBI67, gi:9966869 Submitted (08-MAR-2000) by Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai 200433, P.R. China	Secreted
sbg31848 6-ONC	Oncotrophoblast glycoprotein	GB:AC022045 Submitted (25-JAN-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Canine 5T4 tumour-associated antigen' geneseqp:Y94351 Submitted by OXFORD BIOMEDICA UK LTD Publication number and date: WO200029428-A2, 25-MAY-00	Secreted

Table II (cont.).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg29935 9-LIPO	Lipocalin	SC:AL139041 Submitted (16-NOV-2000) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK	Mouse major urinary protein (MUP) 4, gi:6678968 Shahan K, Gilmartin M, and Derman E; 1987; Mol Cell Biol 7:1938- 1946.	Secreted
sbg23002 2-NGa	Plasmacytoma -associated neuronal glycoprotein	GB:AC066608 GB:AC022002 Submitted (25-APR-2000) and (24-JAN-2000) by Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China	Rat neural cell adhesion protein BIG-2 precursor, gi :1016012 Yoshihara, Y., Kawasaki,M., Tamada,A., Nagata,S., Kagamiyama,H. and Mori,K. J. Neurobiol. 28 (1), 51-69 (1995)	Membrane- bound
sbg29716 9-BGP	Biliary glycoprotein (BGP)	JGI: CITB- E1_2616J11 Submitted by Joint Genome Institute, Department of Energy, USA	Mouse biliary glycoprotein (BGP), gi:312584 McCuaig K, Rosenberg M, Nedellec P, Turbide C, and Beauchemin N; 1993; Gene 127:173- 83.	Secreted
sbg25391 9- HSCCAa	Human squamous cell carcinoma antigen (SCCA)	GB:AC019355 Submitted (02-JAN-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Human squamous cell carcinoma antigen 2 (SCCA-2) (LEUPIN). gi:1710877. Schneider,S.S., Schick,C., Fish,K.E., Miller,E., Pena,J.C., Treter,S.D., Hui,S.M. and Silverman,G.A. Proc. Natl. Acad. Sci. U.S.A. 92 (8), 3147- 3151 (1995).	Secreted
sbg22813 7-OLF	Olfactomedin -related protein	GB:AC022606 Submitted (06- FEB-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Rat neuronal olfactomedin-related protein precursor, gi:3024210 Danielson,P.E., Forss- Petters,S., Battenberg,E.L., deLecea,L., Bloom,F.E., and Sutcliffe,J.G., 1994, J. Neurosci. Res. 38:468- 478.	Secreted

Table II (cont.).

Gene Name	Gen Family	Closest Polynucleotide by homology	Closest Peptide by homology	Cell Localization (by homology)
sbg378514-Netrin	Netrin precursor	SC:BA5N16 Submitted (09-APR-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Mouse Netrin-G1a protein gi:9909148 Nakashiba,T., Ikeda,T., Nishimura,S., Tashiro,K., Honjo,T., Culotti,J.G. and Itohara,S. J. Neurosci. 20 (17), 6540-6550 (2000)	Secreted
sbg253227. mucous matrix glycoprotein (EMMG)	Extracellular mucous matrix glycoprotein (EMMG)	GB:AC011647 Submitted (08-OCT-1999) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Human colon specific protein, geneseqp:Y54368 Submitted by DIADEXUS LLC Publication number and date: WO9960161-A1, 25-NOV-99	Secreted
sbg262831-SIAa	Sialoadhesin	JGI:CITB-E1_3073N11 Found at Joint Genome Institute	Human sialic acid binding immunoglobulin-like lectin 8 long splice variant, gi: 9837433 Foussias,G., Yousef,G.M. and Diamandis,E.P. Biochem. Biophys. Res. Commun. 278 (3), 775-781 (2000)	Secreted
sbg233728-LIPASE	Pancreatic lipase	GB:AC011098 Submitted (01-OCT-1999) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA.	Human pancreatic lipase precursor, gi:126318 Lowe ME, Rosenblum JL, and Strauss AW; 1989; J Biol Chem 264:20042-8.	Secreted
sbg400455.-CRF	C1q-related factor (CRF)	GB:AC024339 Submitted (28-FEB-2000) by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	MouseGliacolin, gi:10566471 Koide,T., Aso,A., Yorihuzi,T. and Nagata,K. J. Biol. Chem. 275 (36), 27957-27963 (2000)	Secreted

Table II (cont.).

Gene Name	Gene Family	Closest Polynucleotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg400612-KINASEa	Protein kinase	GB:AP001615 Submitted (04-APR-2000) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku- ku, Tokyo 160-8582, Japan	Murine protein kinase/ankyrin homologue, geneseqp:Y76079 Submitted by GENESIS RES & DEV CORP LTD Publication number and date: WO9955865-A1 04-NOV-99	Secreted
sbg381373-ACRP	Adipocyte complement-related protein (ACRP30)	JGI:RPCI-11_161M6 Found at Joint Genome Institute, Department of Energy, USA	Human adipocyte Complement-Related Protein (ACRP30R2), geneseqp:Y44487. Submitted by SMITHKLINE BEECHAM CORP Publication number and date: WO9964629-A1, 16- DEC-99	Secreted
sbg401294-MEX-3	MEX-3(IAP)	GB:AC026956 Submitted (25-MAR-2000) by Whitehead Institute/ MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Caenorhabditis elegans MEX-3, gi:1644450 Draper,B.W., Mello,C.C., Bowerman,B., Hardin,J. and Priess,J.R. Cell 87 (2), 205-216 (1996)	Cytosolic (RNA- binding protein)
sbg247722-Cadherin	OB-Cadherin	GB:AL132780 Submitted (02-NOV-1999) by Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE	Human OB-cadherin- 1, gi:1377894 Okazaki,M., Takeshita,S., Kawai,S., Kikuno,R., Tsujimura,A., Kudo,A. and Amann,E. J. Biol. Chem. 269 (16), 12092-12098 (1994)	Secreted

Table II (c nt).

Gene Name	Gene Family	Closest P lnuclotide by homology	Closest Polypeptide by homology	Cell Localization (by homology)
sbg391057-THIPa	Thyroid hormone induced protein	SC:AL158153, SC:AL392044 Submitted (22-MAR-2001) and (02-MAR-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human TANGO 239, geneseqp:B01432 Submitted by MILLENNIUM PHARM INC Publication number and date: WO200039284-A1, 06-JUL-00	Secreted
sbg378067-TGFc	TGF beta (transforming growth factor beta)	SC:AL162502 Submitted (06-APR-2001) by Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK.	Human persephin growth factor, geneseqp:Y16714 Submitted by UNIV WASHINGTON Publication number and date: WO9914235-A1 25-MAR-99	Secreted

Table III.

Gene Name	Uses	Associated Diseases
sbg318680-DNase	An embodiment of the invention is the use of sbg318680-Dnase to treat respiratory diseases and target parasites or cancer cells as a chromosome degrading agent to cause death of those cells. Close homologues of sbg318680-DNase are DNases. DNase can be used to treat respiratory diseases, such as pneumonia, cystic fibrosis and asthma, by reducing viscosity of bronchopulmonary secretions (MacConnachie AM; 1999; <i>Intensive Crit Care Nurs</i> 14:101-2).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation and respiratory diseases
sbg237038-SA	An embodiment of the invention is the use of sbg237038SA in blood pressure control. A close homologue of sbg237038SA is the rat SA gene. The SA gene is expressed at higher levels in the kidney of genetically hypertensive rats (Yang T, Hassan SA, Singh I, Smart A, Brosius FC, Holzman LB, Schnermann JB, Briggs JP; 1996; <i>Hypertension</i> 27:541-51).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and hypertension
sbg340871-GPV	An embodiment of the invention is the use of sbg340871-GPV in hemostasis and platelet aggregation. A close homologue of sbg340871-GPV is platelet glycoprotein (GP) V. Platelet glycoprotein (GP) V is a major surface protein which is cleaved by thrombin during platelet activation, and associates with GPIb-IX complex to form GPIb-V-IX, a receptor for von Willebrand factor and thrombin. Its functional role in hemostasis is possibly related to thrombin-induced platelet aggregation (Ravanat C, Morales M, Azorsa DO, Moog S, Schuhler S, Grunert P, Loew D, Van Dorsselaer A, Cazenave JP, Lanza F; 1997; <i>Blood</i> 89:3253-62).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and Bernard-Soulier disease
sbg293416-HNKS	An embodiment of the invention is the use of sbg293416-HNKS in cell interactions and the development of the nervous system. Close homologues of sbg293416-HNKS are sulfotransferases. Sulfotransferases are considered to be key enzymes in the biosynthesis of the HNK-1 carbohydrate epitope, which is expressed on several neural adhesion glycoproteins and as a glycolipid, and is involved in cell interactions (Bakker,H., Friedmann,I., Oka,S., Kawasaki,T., Nifant'ev,N., Schachner,M. and Mantei,N., 1997, <i>J. Biol. Chem.</i> 272:29942-29946). The HNK-1 epitope is spatially and temporally regulated during the development of the nervous system. The biological function of the HNK-1 sulfotransferase may be related to the development of the nervous system, and also may be involved in the preferential reinnervation of muscle nerves by motor axons after lesion (Jungalwala FB, 1994, <i>Neurochem Res</i> 19:945-57).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and peripheral neuropathies

Table III (c nt).

Gene Name	Uses	Associated Diseases
sbg257418-ZP	An embodiment of the invention is the use of sbg257418ZP in fertilization. A close homologue of sbg257418ZP is zona pellucida. Zona pellucida protein is an extracellular matrix that surrounds growing oocytes, ovulated eggs, and early embryos and it is critically involved in fertilization (Epifano,O., Liang,L.F., Familiari,M., Moos,M.C. Jr. and Dean,J.; 1995; Development 121:1947-1956). The zona pellucida also provides a post-fertilization block to polyspermy and protects the growing embryo as it passes down the oviduct (Rankin T, and Dean J; 1996; Mol Hum Reprod 2:889-94).	Infertility
sbg319185-CDa	An embodiment of the invention is the use of sbg319185CDa, a secreted protein, in the diagnosis and treatment of cancer and autoimmune disorders. Close homologues of sbg319185CDa are leukocyte differentiation antigen CD84 isoforms. CD84's are members of the immunoglobulin superfamily, show high homology with several molecules belonging to the CD2 family of differentiation antigens and is proposed to be useful in the diagnosis and treatment of cancer and autoimmune disorders (Palou E, Pirotto F, Sole J, Freed JH, Peral B, Vilardell C, Vilella R, Vives J, Gaya A. Genomic characterization of CD84 reveals the existence of five isoforms differing in their cytoplasmic domains. <i>Tissue Antigens</i> 2000 Feb;55(2):118-27)).	Cancer, autoimmune disorders, wound healing disorders, infections and hematopoietic disorders
sbg323307-KIAAa	An embodiment of the invention is the use of sbg323307-KIAAa, a secreted protein, to regulate cell signaling, motility, and nucleic acid management. A close homologue of sbg323307-KIAAa is human KIAA0918 protein. Human KIAA0918 protein, a slit-like protein is functionally related to cell signaling/communication, cell structure/motility and nucleic acid management (Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirosawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. KIAA0918 protein [Homo sapiens], <i>DNA Res.</i> 5 (6), 355-364 (1998)).	Cancer, autoimmune disorders, infections, wound healing disorders and hematopoietic disorders

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg315953-GPPa	An embodiment of the invention is the use of sbg315953GPPa, a secreted protein, to treat disorders associated with lipopolysaccharides. A close homologue to sbg315953GPPa is Bovine granulocyte peptide A precursor. Bovine granulocyte peptide A precursors are used in human and veterinary medicine, particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia (1. Selsted ME, Bovine granulocyte peptide A precursor (antimicrobial BGP-A). Accession Number W23722, Publication Date 21-AUG-97. 2. Yount NY, Yuan J, Tarver A, Castro T, Diamond G, Tran PA, Levy JN, McCullough C, Cullor JS, Bevins CL, Selsted ME. Cloning and expression of bovine neutrophil beta-defensins. Biosynthetic profile during neutrophilic maturation and localization of mature peptide to novel cytoplasmic dense granules. <i>J Biol Chem</i> 1999 Sep 10;274(37):26249-58)).	Infections, cancer, autoimmune disorders, wound healing disorders and hematopoietic disorders.
sbg318486-ONC	An embodiment of the invention is the use of sbg318486ONC in the growth and invasion events of trophoblast and tumor cells. A close homologue to sbg318486ONC is oncotrophoblast glycoproteins. It has been shown that oncotrophoblast protein was expressed by tumor cells with metastatic spread, suggesting a role in invasion during cancer (King,K.W., Sheppard,F.C., Westwater,C., Stern,P.L. and Myers,K.A.; 1999; <i>Biochim. Biophys. Acta</i> 1445, 257-270).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation
sbg299359-LIPO	An embodiment of the invention is the use of sbg299359LIPO in sperm maturation, taste recognition, and transportation of some molecules across the blood brain barrier. A close homologue to sbg299359LIPO is Lipocalin. Lipocalins transport small hydrophobic molecules such as steroids, bilins, retinoids, and lipids, and they have various effects on a number of tissues. It has been shown that lipocalins are involved in sperm maturation, taste recognition, and transportation of some molecules across the blood brain barrier (Newcomer M.E.; 1993; <i>Structure</i> 1:7-18; Achen M.G., Harms P.J., Thomas T., Richardson S.J., Wettenhall R.E.H., Schreiber G.; 1992; <i>J. Biol. Chem.</i> 267:23170-23174)	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, and inflammation

Table III (cont.).

Gene Name	Uses	Associated Diseases
sbg230022-NGa	An embodiment of the invention is the use of sbg230022NGa in the formation and maintenance of neuron type-specific networks in the brain. Close homologues to sbg230022NGa are mouse plasmacytoma-associated neuronal glycoprotein and rat BIG-1 protein. Mouse plasmacytoma-associated neuronal glycoprotein, is ectopically activated by intracisternal A-type particle long terminal repeats in murine plasmacytomas. Rat BIG-1 protein, is a TAG-1/F3-related member of the immunoglobulin superfamily with neurite outgrowth-promoting activity and involved in the formation and maintenance of neuron type-specific networks in the brain (1. Connelly MA, Grady RC, Mushinski JF, Marcu KB. PANG, a gene encoding a neuronal glycoprotein, is ectopically activated by intracisternal A-type particle long terminal repeats in murine plasmacytomas. Proc Natl Acad Sci U S A 1994 Feb 15;91(4):1337-41 2. Yoshihara Y, Kawasaki M, Tani A, Tamada A, Nagata S, Kagamiyama H, Mori K. BIG-1: a new TAG-1/F3-related member of the immunoglobulin superfamily with neurite outgrowth-promoting activity. Neuron 1994 Aug;13(2):415-26).	Cancer, infections, autoimmune disorders, wound healing disorders and hematopoietic disorders
sbg297169-BGP	An embodiment of the invention is the use of sbg297169BGP in renewal and/or differentiation of epithelial cells. A close homologue to sbg297169BGP is BGP protein. BGP proteins are expressed at the cell surface and function <i>in vitro</i> as cell adhesion molecules. The expression of the many BGP isoforms at the surface of epithelial cells, such as the colon, suggests that these proteins play a major role in renewal and/or differentiation of their epithelia (McCuaig K, Rosenberg M, Nedellec P, Turbide C, and Beauchemin N; 1993; Gene 127:173-83).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg253919-HSCCAa	An embodiment of the invention is the use of sbg253919-HSCCAa for treatment of cancer or psoriasis or in development of more aggressive squamous cell carcinomas. Close homologues of sbg253919-HSCCAa are Psoriastatin type II and a human leupin precursor. Psoriastatin type II, is claimed to modulate activity of psoriastatin type I and II genes, e.g. using (ant)agonists, useful for treatment of cancer or psoriasis. The other, a human leupin precursor, contains a tandem duplication of the human squamous cell carcinoma antigen gene playing a causal role in development of more aggressive squamous cell carcinomas (1. Goetinck PF, Hibino T, Takahashi T and Baciu PC. Modulating cell proliferation or apoptosis - by modulating activity of psoriastatin type I and II genes, e.g. using (ant) agonists, useful for treatment of cancer or psoriasis. Accession Number W15242, publication date 24-APR-97. 2. Schneider SS, Schick C, Fish KE, Miller E, Pena JC, Treter SD, Hui SM, Silverman GA. A serine proteinase inhibitor locus at 18q21.3 contains a tandem duplication of the human squamous cell carcinoma antigen gene. Proc Natl Acad Sci U S A 1995 Apr 11;92(8):3147-51. 3. Barnes RC, Worrall DM. Identification of a novel human serpin gene; cloning sequencing and expression of leupin. FEBS Lett 1995 Oct 2; 373 (1): 61-5).	Cancers, such as squamous cell carcinomas
sbg228137-OLF	An embodiment of the invention is the use of sbg228137OLF in functional roles in chemoreception and in the central nervous system. A close homologue to sbg228137OLF is olfactomedin. Olfactomedin is a glycoprotein, and reacts with proteins of olfactory cilia. It was originally discovered at the mucociliary surface of the amphibian olfactory neuroepithelium and subsequently found throughout the mammalian brain (Danielson, P.E., Forss-Petter, S., Battenberg, E.L., deLecea, L., Bloom, F.E., and Sutcliffe, J.G., 1994, J. Neurosci. Res. 38:468-478). Its noticeable deposition at the chemosensory surface of the olfactory neuroepithelium suggests a role for this protein in chemoreception (Snyder DA, Rivers AM, Yokoe H, Menco BP, and Anholt RR, 1991, Biochemistry 30:9143-53). The widespread occurrence of olfactomedin among mammals in the brains also suggests its new functions in the central nervous system (Karavanich CA, and Anholt RR, 1998, Mol Biol Evol 15:718-26).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and nervous system disorders

Table III (c nt).

Gen Name	Uses	Associated Diseases
sbg378514-Netrin	An embodiment of the invention is the use of sbg378514-Netrin in roles of the central nervous system. A close homologue to sbg378514-Netrin is Netrin. Netrins possess commissural axon outgrowth-promoting activity, and control guidance of CNS commissural axons and peripheral motor axons (Serafini T, Kennedy TE, Galko MJ, Mirzayan C, Jessell TM, and Tessier-Lavigne M; 1994; <i>Cell</i> 78:409-24). Diffusible and substrate-bound cues, including netrins and their receptors, can guide axonal pathway choice via attractive and repulsive signals (Tear G; 1998; <i>Essays Biochem</i> 33:1-13).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and nervous system disorder
sbg253227. mucous matrix glycoprotein	An embodiment of the invention is the use of sbg253227.-mucous matrix glycoprotein for the treatment of gastrointestinal disorders and cancer. Close homologues of sbg253227.mucous matrix glycoprotein have been used in combination for treatment of infections associated with EMMG. EMMG is useful for the treatment of gastrointestinal disorders and cancer, e.g. dysphagia, abdominal angina, pancreatitis, colonic carcinoma, Crohn's disease and the Mallory-Weiss syndrome (US5929033-A, CORLEY NC, TANG YT, Submitted by INCYTE PHARM INC. Reference number, WPI; 99-429518/36, 1999).	Hematopoietic disorder, wound healing disorder, viral and bacterial infection, cancer, autoimmune diseases Neurological disorders, gastrointestinal disorders,dysphagia, abdominal angina, pancreatitis, colonic carcinoma,Crohn's disease and the Mallory-Weiss syndrome.
sbg262831-SIAa	An embodiment of the invention is the use of sbg262831SIAa to mediate sialic acid-dependent ligand recognition and to function as an inhibitory receptor in human natural killer cells. A close homologue of sbg262831SIAa is human QA79 membrane protein. QA79 belongs to the sialoadhesin family and is proposed to mediate sialic acid-dependent ligand recognition and to function as an inhibitory receptor in human natural killer cells (Falco,M., Biassoni,R., Bottino,C., Vitale,M., Sivori,S., Augugliaro,R., Moretta,L. and Moretta,A. Identification and molecular cloning of p75/AIRM1, a novel member of the sialoadhesin family that functions as an inhibitory receptor in human natural killer cells. <i>J Exp Med</i> 1999 Sep 20;190(6):793-802).	Cancer, autoimmune disorders, infection, wound healing disorders, and hematopoietic disorders.

Table III (cont).

Gene Name	Uses	Associated Diseases
sbg233728-LIPASE	An embodiment of the invention is the use of sbg233728LIPASE to treat pancreatitis via replacement therapy. A close homologue of sbg233728-LIPASE is pancreatic lipase. Pancreatic lipase can be used as replacement enzymes for patients with chronic pancreatitis. Pancreatic lipase hydrolyzes dietary long chain triacylglycerol to free fatty acids and monoacylglycerols in the intestinal lumen (Lowe ME, Rosenblum JL, and Strauss AW; 1989; <i>J Biol Chem</i> 264:20042-8). Pancreatic steatorrhea and pancreatic diabetes are the dominant symptoms of patients in a certain stage of chronic pancreatitis. In this stage, the nutritional state is greatly disturbed and hypoglycemia and labile infection are involved. Pancreatic enzyme replacement therapy is the principal treatment method for pancreatic steatorrhea. (Nakamura T, Takeuchi T, and Tando Y; 1998; <i>Pancreas</i> 16:329-36).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, and pancreatitis.
sbg400455-CRF	An embodiment of the invention is the use of sbg400455.CRF in the areas of the nervous system involved in motor function, such as the Purkinje cells of the cerebellum, the accessory olfactory nucleus, the pons, and the red nucleus. Close homologues of sbg400455.CRF include CRF transcripts. CRF transcripts are most abundant in areas of the nervous system and have been used to develop products for modulating energy balance or insulin production in mammals ((W09639429-A2) Schere, P.E.; Submitted by Whithead Institute of Biomedical Research; Berube NG, Swanson XH, Bertram MJ, Kittle JD, Didenko V, Baskin DS, Smith JR and Pereira-Smith OM., <i>Brain Res. Mol. Brain Res.</i> 63 (2), 233-240 (1999)).	Hematopoietic disorder, wound healing disorder, viral and bacterial infection, cancer, autoimmune diseases, energy homeostasis disorder and obesity
sbg400612-KINASEa	An embodiment of the invention is the use of sbg400612-KINASEa in the treatment of inflammation, cancer, neurological diseases, growth and developmental defects, skin wounds, and hair follicle disorders. A close homologue of sbg400612-KINASEa is murine protein kinase/ ankyrin homologue. Murine protein kinase/ ankyrin homologue can stimulate the growth and motility of keratinocytes, inhibit the growth of cancer cells, modulate angiogenesis and tumour vascularisation, modulate skin inflammation and epithelial cell growth and inhibit binding of HIV-1 to leukocytes. Murine protein kinase/ ankyrin homologue can also be used to treat inflammation, cancer, neurological diseases, growth and developmental defects, skin wounds, and hair follicle disorders (Kumble A, Murison JG, Onrust R, Sleeman M, Strachan L and Watson JD. Novel polynucleotides useful for the treatment of various conditions including wounds and cancer. Accession Number: Y76079 Publication Date: 04-NOV-99).	Cancer, wound healing disorders, autoimmune disorders, hematopoietic disorders and infection

Table III (cont.).

Gen Name	Uses	Associated Diseases
sbg381373-ACRP	An embodiment of the invention is the use of sbg381373-ACRP in the complex balanced system of energy homeostasis involving food intake, carbohydrate catabolism, and lipid catabolism. A close homologue of sbg381373-ACRP is ACRP30 protein. ACRP30 protein may be a factor that participates in the complex balanced system of energy homeostasis involving food intake, carbohydrate catabolism, and lipid catabolism. ACRP30 is structurally similar to complement factor C1q, and it forms large homo-oligomers that undergo a series of post-translational modifications (Scherer PE, Williams S, Fogliano M, Baldini G, Lodish HF; 1995; <i>J Biol Chem</i> 270:26746-9).	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorders, inflammation, obesity, and diabetes
sbg401294-MEX-3	An embodiment of the invention is the use of sbg401294-MEX-3 to develop products for diagnosis and therapy of disease states such as tumor formation, apoptosis regulation in cells to reduce or increase apoptosis and for pharmacological screening.	Hematopoietic disorder, wound healing disorder, viral and bacterial infection, cancer, tumor formation, autoimmune diseases, inhibition of apoptosis
sbg247722-Cadherin	An embodiment of the invention is the use of sbg247722-Cadherin for treatment and diagnosis of bone metabolic diseases. A close homologue of sbg247722-Cadherin is cadherin, a Ca ²⁺ dependent cell adhesion protein.	Hematopoietic disorder, wound healing disorder, viral and bacterial infection, cancer, autoimmune diseases, energy homeostasis disorder and bone metabolic disease
sbg391057-THIPa	An embodiment of the invention is the use of sbg391057-THIPa in controlling thyroid hormone synthesis. A close homologue of sbg391057-THIPa is <i>xenopus laevis</i> thyroid hormone-induced protein. <i>Xenopus laevis</i> thyroid hormone-induced protein has been implicated in controlling thyroid hormone synthesis in <i>Xenopus</i> tadpoles and provided insights into the biology of metamorphosis (Brown,D.D., Wang,Z., Furlow,J.D., Kanamori,A., Schwartzman, R.A., Remo,B.F. and Pinder,A. The thyroid hormone-induced tail resorption program during <i>Xenopus laevis</i> metamorphosis. <i>Proc Natl Acad Sci U S A</i> 1996 Mar 5;93(5):1924-9).	Autoimmune disorders, wound healing disorders, cancer, infection and hematopoietic disorders

Table III (continued).

Gene Name	Uses	Associated Diseases
sbg378067-TGF β	An embodiment of the invention is the use of sbg378067-TGF β in cellular growth control in the etiology of cancer and cell differentiation and development. The sbg378067-TGF β protein contains a close approximation of the prosite consensus pattern (PDOC00223) for TGF- β family members. TGF- β proteins have been known to be involved in growth control and hence the etiology of cancer (<i>Anticancer Res</i> 1999 Nov-Dec;19(6A):4791-807), cell differentiation and development. A TGF- β signaling pathway constitutes a tumor suppressor path (<i>Cytokine Growth Factor Rev</i> 2000 Apr 1;11(1-2):159-168). A close homologue of sbg378067-TGF β is TGF- β protein.	Cancer, infection, autoimmune disorder, hematopoietic disorder, wound healing disorder, inflammation, preventing or treating cellular degeneration or insufficiency, e.g. neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumours, multiple sclerosis, or infection (viral, bacterial, fungal, parasitic), hematopoietic cell degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiencies, cardiac muscle degeneration or insufficiency resulting from cardiomyopathy or congestive heart failure, peripheral nerve trauma or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents

Table IV. Quantitative, Tissue-specific mRNA expression detected using SybrMan

Quantitative, tissue-specific, mRNA expression patterns of the genes were measured using SYBR-Green Quantitative PCR (Applied Biosystems, Foster City, CA; see Schmittgen T.D. et al., Analytical Biochemistry 285:194-204, 2000) and human cDNAs prepared from various human

5 tissues. Gene-specific PCR primers were designed using the first nucleic acid sequence listed in the Sequence List for each gene. Results are presented as the number of copies of each specific gene's mRNA detected in 1ng mRNA pool from each tissue. Two replicate mRNA measurements were made from each tissue RNA.

Gene Name	Tissue-Specific mRNA Expression (copies per ng mRNA; avg. \pm range for 2 data points per tissue)									
	Brain	Heart	Lung	Liver	Kidney	Skeletal muscle	Intestine	Spleen/lymph	Placenta	Testis
sbg237038SA	14 \pm 1	27 \pm 1	39 \pm 1	14 \pm 0	18 \pm 1	12 \pm 0	21 \pm 3	45 \pm 2	19 \pm 3	40 \pm 9
sbg340871-GPV	0 \pm 0	200 \pm 46	363 \pm 10	-9 \pm 6	33 \pm 13	93 \pm 17	74 \pm 9	305 \pm 9	2902 \pm 114	36 \pm 4
sbg293416-HNKS	553 \pm 15	65 \pm 1	39 \pm 4	27 \pm 4	39 \pm 1	38 \pm 1	53 \pm 4	225 \pm 9	43 \pm 0	108 \pm 9
sbg257418ZP	37 \pm 3	28 \pm 6	6 \pm 0	-12 \pm 3	-4 \pm 2	19 \pm 7	15 \pm 2	5 \pm 2	10 \pm 2	605 \pm 10
sbg319185-CDa	54 \pm 5	113 \pm 3	696 \pm 140	95 \pm 37	317 \pm 31	708 \pm 30	540 \pm 64	5987 \pm 158	326 \pm 2	258 \pm 31
sbg323307-KIAAa	293 \pm 8	633 \pm 15	1269 \pm 58	15 \pm 1	136 \pm 5	26 \pm 6	1400 \pm 91	33 \pm 12	632 \pm 12	196 \pm 10
sbg315953-GPPa	232 \pm 31	16 \pm 0	54 \pm 2	1 \pm 6	14 \pm 7	4 \pm 8	15 \pm 3	99 \pm 4	61 \pm 7	126 \pm 6
sbg318486-ONC	52 \pm 7	3 \pm 2	8 \pm 0	4 \pm 0	4 \pm 2	2 \pm 1	6 \pm 2	1 \pm 7	4 \pm 1	122 \pm 9
sbg299359-LIPO	1701 \pm 95	39 \pm 0	60 \pm 14	21 \pm 1	135 \pm 13	41 \pm 3	49 \pm 2	26 \pm 7	40 \pm 5	138 \pm 2

Table IV (cont.)

Gene Name	Tissue-Specific mRNA Expression (copies per ng mRNA; avg. \pm range for 2 data points per tissue)									
	Brain	Heart	Lung	Liver	Kidney	Skeletal muscle	Intestine	Spleen/Lymph	Placenta	Testis
sbg230022-NGa	3443 \pm 112	684 \pm 2	386 \pm 7	712 \pm 16	1956 \pm 63	36 \pm 0	588 \pm 7	1293 \pm 17	43 \pm 7	358 \pm 2
sbg297169-BGP	417 \pm 29	141 \pm 8	236 \pm 5	170 \pm 11	322 \pm 0	74 \pm 4	231 \pm 1	370 \pm 0	223 \pm 3	968 \pm 32
sbg253919-HSCCAa	-5 \pm 1	1 \pm 1	2 \pm 1	-14 \pm 2	-10 \pm 0	-4 \pm 3	0 \pm 1	6 \pm 1	4 \pm 3	119 \pm 9
sbg228137-OLF	5174 \pm 138	58 \pm 4	99 \pm 5	9 \pm 3	63 \pm 7	167 \pm 12	98 \pm 0	719 \pm 9	32 \pm 8	67 \pm 4
sbg253227. mucous matrix glycoprotein	5 \pm 0	11 \pm 1	21 \pm 1	0 \pm 1	28 \pm 2	1 \pm 0	13 \pm 2	24 \pm 3	26 \pm 4	118 \pm 1
sbg262831-SIAa	9 \pm 1	6 \pm 1	59 \pm 1	59 \pm 1	5 \pm 0	-4 \pm 2	134 \pm 6	2657 \pm 97	45 \pm 4	25 \pm 0
sbg233728-LIPASE	2 \pm 1	6 \pm 1	4 \pm 2	6 \pm 2	1 \pm 0	4 \pm 0	1 \pm 3	1 \pm 2	3 \pm 2	28 \pm 3
sbg400455.-CRF	8735 \pm 257	345 \pm 14	434 \pm 54	191 \pm 14	4038 \pm 147	705 \pm 32	379 \pm 1	847 \pm 59	434 \pm 8	97 \pm 8
sbg400612-KINASEa	10 \pm 0	24 \pm 4	276 \pm 87	145 \pm 2	431 \pm 10	7 \pm 0	59 \pm 5	23 \pm 4	82 \pm 9	34 \pm 3
sbg381373-ACRP	112 \pm 40	11 \pm 3	15 \pm 5	14 \pm 5	10 \pm 2	11 \pm 8	14 \pm 4	-3 \pm 8	6 \pm 2	11 \pm 8
sbg401294-MEX-3	49 \pm 8	39 \pm 2	122 \pm 1	35 \pm 9	151 \pm 8	6 \pm 5	16 \pm 1	15 \pm 3	71 \pm 8	683 \pm 56
sbg247722-Cadherin	2626 \pm 18	1140 \pm 22	1733 \pm 62	78 \pm 4	2007 \pm 12	213 \pm 52	1175 \pm 47	1701 \pm 167	3487 \pm 263	1814 \pm 30
sbg391057-THIPa	332 \pm 3	3010 \pm 30	8567 \pm 84	136 \pm 1	1013 \pm 90	1499 \pm 172	2469 \pm 86	3512 \pm 23	1393 \pm 32	2408 \pm 174
sbg378067-TGFc	33 \pm 8	58 \pm 6	52 \pm 4	3 \pm 1	48 \pm 1	49 \pm 22	21 \pm 4	116 \pm 28	74 \pm 2	59 \pm 4

Table V. Additional diseases based on mRNA expression in specific tissues

Tissue Expression	Additional Diseases
Brain	Neurological and psychiatric diseases, including Alzheimers, parasupranuclear palsey, Huntington's disease, myotonic dystrophy, anorexia, depression, schizophrenia, headache, amnesias, anxiety disorders, sleep disorders, multiple sclerosis
Heart	Cardiovascular diseases, including congestive heart failure, dilated cardiomyopathy, cardiac arrhythmias, Hodgson's Disease, myocardial infarction, cardiac arrhythmias
Lung	Respiratory diseases, including asthma, Chronic Obstructive Pulmonary Disease, cystic fibrosis, acute bronchitis, adult respiratory distress syndrome
Liver	Dyslipidemia, hypercholesterolemia, hypertriglyceridemia, cirrhosis, hepatic encephalopathy, fatty hepatocirrhosis, viral and nonviral hepatitis, Type II Diabetes Mellitis, impaired glucose tolerance
Kidney	Renal diseases, including acute and chronic renal failure, acute tubular necrosis, cystinuria, Fanconi's Syndrome, glomerulonephritis, renal cell carcinoma, renovascular hypertension
Skeletal muscle	Eulenburg's Disease, hypoglycemia, obesity, tendinitis, periodic paralyses, malignant hyperthermia, paramyotonia congenita, myotonia congenita
Intestine	Gastrointestinal diseases, including Myotonia congenita, Ileus, Intestinal Obstruction, Tropical Sprue, Pseudomembranous Enterocolitis
Spleen/lymph	Lymphangiectasia, hypersplenism, angiomas, ankylosing spondylitis, Hodgkin's Disease, macroglobulinemia, malignant lymphomas, rheumatoid arthritis
Placenta	Choriocarcinoma, hydatidiform mole, placenta previa
Testis	Testicular cancer, male reproductive diseases, including low testosterone and male infertility
Pancreas	Diabetic ketoacidosis, Type 1 & 2 diabetes, obesity, impaired glucose tolerance

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - (a) an isolated polypeptide encoded by a polynucleotide comprising a sequence set forth in Table I;
 - (b) an isolated polypeptide comprising a polypeptide sequence set forth in Table I; and
 - (c) a polypeptide sequence of a gene set forth in Table I.
2. An isolated polynucleotide selected from the group consisting of:
 - (a) an isolated polynucleotide comprising a polynucleotide sequence set forth in Table I;
 - (b) an isolated polynucleotide of a gene set forth in Table I;
 - (c) an isolated polynucleotide comprising a polynucleotide sequence encoding a polypeptide set forth in Table I;
 - (d) an isolated polynucleotide encoding a polypeptide set forth in Table I;
 - (e) a polynucleotide which is an RNA equivalent of the polynucleotide of (a) to (d); or a polynucleotide sequence complementary to said isolated polynucleotide.
3. An expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 when said expression vector is present in a compatible host cell.
4. A process for producing a recombinant host cell which comprises the step of introducing an expression vector comprising a polynucleotide capable of producing a polypeptide of claim 1 into a cell such that the host cell, under appropriate culture conditions, produces said polypeptide.
5. A recombinant host cell produced by the process of claim 4.
6. A membrane of a recombinant host cell of claim 5 expressing said polypeptide.
7. A process for producing a polypeptide which comprises culturing a host cell of claim 5 under conditions sufficient for the production of said polypeptide and recovering said polypeptide from the culture.

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 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 32

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 <212> DNA
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<400> 33

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 <212> DNA
 <213> Homo sapiens

<400> 34

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 <211> 1824
 <212> DNA

<213> Homo sapiens

<400> 35

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<210> 36

<211> 2346

<212> DNA

<213> Homo sapiens

<400> 36

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 <211> 1923
 <212> DNA
 <213> Homo sapiens

<400> 37						
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<212> DNA
<213> *Homo sapiens*

<400> 38

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<212> DNA
<213> *Homo sapiens*

<400> 39

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465

<210> 40
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 40
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 35 40 45
 Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val Val Asp Ser Ser Gln
 50 55 60
 Asn Thr Val Pro Phe Leu Leu Gln Lys Leu Lys Ser Ser Arg Ser Tyr
 65 70 75 80
 Ser Phe Leu Asn Ser Ser Leu Leu Gly Arg Ser Thr Tyr Lys Glu Lys
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 Asp Val Phe Leu Asp Val Tyr Gln Arg Trp Gln Asn Glu Asn Val Ile
 165 170 175
 Leu Leu Gly Asp Phe Asn Ala Asp Cys Ala Ser Leu Thr Lys Lys Arg
 180 185 190
 Leu Lys Ser Leu Leu Leu Arg Thr Lys Ala Gly Phe His Trp Val Ile
 195 200 205
 Pro Asp Gly Glu Asp Thr Thr Val Arg Ala Ser Thr Asn Cys Thr Tyr
 210 215 220
 Asp Arg Ile Val Val His Gly Gln Gly Cys Gln Met Leu Leu Lys Ala
 225 230 235 240
 Ala Ala Thr Phe Asp Phe Pro Lys Arg Phe Gln Leu Thr Glu Glu Glu
 245 250 255
 Ala Leu Arg Ile Ser Asp His Tyr Pro Val Glu Val Glu Leu Ser Gln
 260 265 270
 Ala Thr Pro Leu Ser
 275

<210> 41
 <211> 480
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Leu Gly Arg Phe Gln Pro Phe Ser Leu Val Arg Ser Phe Arg Leu
 1 5 10 15
 Gly Phe Gly Ala Cys Cys Tyr Pro Asn Gln Lys Cys Ala Thr Gln Thr
 20 25 30
 Ile Arg Pro Pro Asp Ser Arg Cys Leu Val Gln Ala Val Ser Gln Asn
 35 40 45
 Phe Asn Phe Ala Lys Asp Val Leu Asp Gln Trp Ser Gln Leu Glu Lys
 50 55 60

Asp Gly Leu Arg Gly Pro Tyr Pro Ala Leu Trp Lys Val Ser Ala Lys
 65 70 75 80
 Gly Glu Glu Asp Lys Trp Ser Phe Glu Arg Met Thr Gln Leu Ser Lys
 85 90 95
 Lys Ala Ala Ser Ile Leu Ser Asp Thr Cys Ala Leu Ser His Gly Asp
 100 105 110
 Arg Leu Met Ile Ile Leu Pro Pro Thr Pro Glu Ala Tyr Trp Ile Cys
 115 120 125
 Leu Ala Cys Val Arg Leu Gly Ile Thr Phe Val Pro Gly Ser Pro Gln
 130 135 140
 Leu Thr Ala Lys Lys Ile Arg Tyr Gln Leu Arg Met Ser Lys Ala Gln
 145 150 155 160
 Cys Ile Val Ala Asn Glu Ala Met Ala Pro Val Val Asn Ser Ala Val
 165 170 175
 Ser Asp Cys Pro Thr Leu Lys Thr Lys Leu Leu Val Ser Asp Lys Ser
 180 185 190
 Tyr Asp Gly Trp Leu Asp Phe Lys Lys Leu Ile Gln Val Ala Pro Pro
 195 200 205
 Lys Gln Thr Tyr Met Arg Thr Lys Ser Gln Asp Pro Met Ala Ile Phe
 210 215 220
 Phe Thr Lys Gly Thr Thr Gly Ala Pro Lys Met Val Glu Tyr Ser Gln
 225 230 235 240
 Tyr Gly Leu Gly Met Gly Phe Ser Gln Ala Ser Arg Arg Trp Met Asp
 245 250 255
 Leu Gln Pro Thr Asp Val Leu Trp Ser Leu Gly Asp Ala Phe Gly Gly
 260 265 270
 Ser Leu Ser Leu Ser Ala Val Leu Gly Thr Trp Phe Gln Gly Ala Cys
 275 280 285
 Val Phe Leu Cys His Met Pro Thr Phe Cys Pro Glu Thr Val Leu Asn
 290 295 300
 Val Leu Ser Arg Phe Pro Ile Thr Thr Leu Ser Ala Asn Pro Glu Met
 305 310 315 320
 Tyr Gln Glu Leu Leu Gln His Lys Cys Phe Thr Ser Tyr Arg Phe Lys
 325 330 335
 Ser Leu Lys Gln Cys Val Ala Ala Gly Gly Pro Ile Ser Pro Gly Val
 340 345 350
 Ile Glu Asp Trp Lys Arg Ile Thr Lys Leu Asp Ile Tyr Glu Gly Tyr
 355 360 365
 Gly Gln Thr Glu Thr Gly Leu Leu Cys Ala Thr Ser Lys Thr Ile Lys
 370 375 380
 Leu Lys Pro Ser Ser Leu Gly Lys Pro Leu Pro Pro Tyr Ile Val Gln
 385 390 395 400
 Ile Val Asp Glu Asn Ser Asn Leu Leu Pro Pro Gly Glu Glu Gly Asn
 405 410 415
 Ile Ala Ile Arg Ile Lys Leu Asn Gln Pro Ala Ser Leu Tyr Cys Pro
 420 425 430
 His Met Val Ser Trp Glu Glu Tyr Ala Ser Ala Arg Gly His Met Leu
 435 440 445
 Tyr Leu Thr Gly Asp Arg Gly Ile Met Asp Glu Asp Gly Tyr Phe Trp
 450 455 460
 Trp Ser Gly Arg Val Asp Asp Val Ala Asn Ala Leu Gly Gln Arg Leu
 465 470 475 480

<210> 42
 <211> 583
 <212> PRT
 <213> Homo sapiens

<400> 42

Met Leu Gly Arg Phe Gln Pro Phe Ser Leu Val Arg Ser Phe Arg Leu
 1 5 10 15
 Gly Phe Gly Ala Cys Cys Tyr Pro Asn Gln Lys Cys Ala Thr Gln Thr
 20 25 30
 Ile Arg Pro Pro Asp Ser Arg Cys Leu Val Gln Ala Val Ser Gln Asn
 35 40 45
 Phe Asn Phe Ala Lys Asp Val Leu Asp Gln Trp Ser Gln Leu Glu Lys
 50 55 60
 Asp Gly Leu Arg Gly Pro Tyr Pro Ala Leu Trp Lys Val Ser Ala Lys
 65 70 75 80
 Gly Glu Glu Asp Lys Trp Ser Phe Glu Arg Met Thr Gln Leu Ser Lys
 85 90 95
 Lys Ala Ala Ser Ile Leu Ser Asp Thr Cys Ala Leu Ser His Gly Asp
 100 105 110
 Arg Leu Met Ile Ile Leu Pro Pro Thr Pro Glu Ala Tyr Trp Ile Cys
 115 120 125
 Leu Ala Cys Val Arg Leu Gly Ile Thr Phe Val Pro Gly Ser Pro Gln
 130 135 140
 Leu Thr Ala Lys Lys Ile Arg Tyr Gln Leu Arg Met Ser Lys Ala Gln
 145 150 155 160
 Cys Ile Val Ala Asn Glu Ala Met Ala Pro Val Val Asn Ser Ala Val
 165 170 175
 Ser Asp Cys Pro Thr Leu Lys Thr Lys Leu Leu Val Ser Asp Lys Ser
 180 185 190
 Tyr Asp Gly Trp Leu Asp Phe Lys Lys Leu Ile Gln Val Ala Pro Pro
 195 200 205
 Lys Gln Thr Tyr Met Arg Thr Lys Ser Gln Asp Pro Met Ala Ile Phe
 210 215 220
 Phe Thr Lys Gly Thr Thr Gly Ala Pro Lys Met Val Glu Tyr Ser Gln
 225 230 235 240
 Tyr Gly Leu Gly Met Gly Phe Ser Gln Ala Ser Arg Arg Trp Met Asp
 245 250 255
 Leu Gln Pro Thr Asp Val Leu Trp Ser Leu Gly Asp Ala Phe Gly Gly
 260 265 270
 Ser Leu Ser Leu Ser Ala Val Leu Gly Thr Trp Phe Gln Gly Ala Cys
 275 280 285
 Val Phe Leu Cys His Met Pro Thr Phe Cys Pro Glu Thr Val Leu Asn
 290 295 300
 Val Leu Ser Arg Phe Pro Ile Thr Thr Leu Ser Ala Asn Pro Glu Met
 305 310 315 320
 Tyr Gln Glu Leu Leu Gln His Lys Cys Phe Thr Ser Tyr Arg Phe Lys
 325 330 335
 Ser Leu Lys Gln Cys Val Ala Ala Gly Gly Pro Ile Ser Pro Gly Val
 340 345 350
 Ile Glu Asp Trp Lys Arg Ile Thr Lys Leu Asp Ile Tyr Glu Gly Tyr
 355 360 365
 Gly Gln Thr Glu Thr Gly Leu Leu Cys Ala Thr Ser Lys Thr Ile Lys
 370 375 380
 Leu Lys Pro Ser Ser Leu Gly Lys Pro Leu Pro Pro Tyr Ile Val Gln
 385 390 395 400
 Ile Val Asp Glu Asn Ser Asn Leu Leu Pro Pro Gly Glu Glu Gly Asn
 405 410 415
 Ile Ala Ile Arg Ile Lys Leu Asn Gln Pro Ala Ser Leu Tyr Cys Pro
 420 425 430
 His Met Val Ser Trp Glu Glu Tyr Ala Ser Ala Arg Gly His Met Leu
 435 440 445
 Tyr Leu Thr Gly Asp Arg Gly Ile Met Asp Glu Asp Gly Tyr Phe Trp
 450 455 460
 Trp Ser Gly Arg Val Asp Asp Val Ala Asn Ala Leu Gly Gln Arg Phe

465	470	475	480
Ser Arg Pro Gly Ala Ala Ala Ala Ala Ser	Ala Val Gly Ala Pro Pro		
485	490	495	
Gly Gly Trp His Ser Leu Cys Ala Ser Val Pro Ile Leu Gln Val Val			
500	505	510	
Lys Pro Pro Asn Val Leu Thr Pro Gln Phe Leu Ser His Asp Gln Gly			
515	520	525	
Gln Leu Thr Lys Glu Leu Gln Gln His Ile Lys Ser Val Thr Gly Pro			
530	535	540	
Cys Lys Tyr Gln Arg Lys Val Glu Phe Val Pro Glu Leu Pro Lys Thr			
545	550	555	560
Val Thr Gly Lys Ile Lys Arg Glu Leu Gln Val Trp Ser Asp Val Val			
565	570		575
Ser Ser Glu Leu Arg Asn Asp			
580			

<210> 43
 <211> 581
 <212> PRT
 <213> Homo sapiens

<400> 43			
Met Pro Leu Lys His Tyr Leu Leu Leu Leu Val Gly Cys Gln Ala Trp			
1	5	10	15
Gly Ala Gly Leu Ala Tyr His Gly Cys Pro Ser Glu Cys Thr Cys Ser			
20	25	30	
Arg Ala Ser Gln Val Glu Cys Thr Gly Ala Arg Ile Val Ala Val Pro			
35	40	45	
Thr Pro Leu Pro Trp Asn Ala Met Ser Leu Gln Ile Leu Asn Thr His			
50	55	60	
Ile Thr Glu Leu Asn Glu Ser Pro Phe Leu Asn Ile Ser Ala Leu Ile			
65	70	75	80
Ala Leu Arg Ile Glu Lys Asn Glu Leu Ser Arg Ile Thr Pro Gly Ala			
85	90	95	
Phe Arg Asn Leu Gly Ser Leu Arg Tyr Leu Ser Leu Ala Asn Asn Lys			
100	105	110	
Leu Gln Val Leu Pro Ile Gly Leu Phe Gln Gly Leu Asp Ser Leu Glu			
115	120	125	
Ser Leu Leu Leu Ser Ser Asn Gln Leu Leu Gln Ile Gln Pro Ala His			
130	135	140	
Phe Ser Gln Cys Ser Asn Leu Lys Glu Leu Gln Leu His Gly Asn His			
145	150	155	160
Leu Glu Tyr Ile Pro Asp Gly Ala Phe Asp His Leu Val Gly Leu Thr			
165	170	175	
Lys Leu Asn Leu Gly Lys Asn Ser Leu Thr His Ile Ser Pro Arg Val			
180	185	190	
Phe Gln His Leu Gly Asn Leu Gln Val Leu Arg Leu Tyr Glu Asn Arg			
195	200	205	
Leu Thr Asp Ile Pro Met Gly Thr Phe Asp Gly Leu Val Asn Leu Gln			
210	215	220	
Glu Leu Ala Leu Gln Gln Asn Gln Ile Gly Leu Leu Ser Pro Gly Leu			
225	230	235	240
Phe His Asn Asn His Asn Leu Gln Arg Leu Tyr Leu Ser Asn Asn His			
245	250	255	
Ile Ser Gln Leu Pro Pro Ser Ile Phe Met Gln Leu Pro Gln Leu Asn			
260	265	270	
Arg Leu Thr Leu Phe Gly Asn Ser Leu Lys Glu Leu Ser Leu Gly Ile			
275	280	285	
Phe Gly Pro Met Pro Asn Leu Arg Glu Leu Trp Leu Tyr Asp Asn His			

290	295	300
Ile Ser Ser Leu Pro Asp Asn Val Phe Ser Asn Leu Arg Gln Leu Gln		
305	310	315
Val Leu Ile Leu Ser Arg Asn Gln Ile Ser Phe Ile Ser Pro Gly Ala		320
325	330	335
Phe Asn Gly Leu Thr Glu Leu Arg Glu Leu Ser Leu His Thr Asn Ala		
340	345	350
Leu Gln Asp Leu Asp Gly Asn Val Phe Arg Met Leu Ala Asn Leu Gln		
355	360	365
Asn Ile Ser Leu Gln Asn Asn Arg Leu Arg Gln Leu Pro Gly Asn Ile		
370	375	380
Phe Ala Asn Val Asn Gly Leu Met Ala Ile Gln Leu Gln Asn Asn Gln		
385	390	395
Leu Glu Asn Leu Pro Leu Gly Ile Phe Asp His Leu Gly Lys Leu Cys		400
405	410	415
Glu Leu Arg Leu Tyr Asp Asn Pro Trp Arg Cys Asp Ser Asp Ile Leu		
420	425	430
Pro Leu Arg Asn Trp Leu Leu Leu Asn Gln Pro Arg Leu Gly Thr Asp		
435	440	445
Thr Val Pro Val Cys Phe Ser Pro Ala Asn Val Arg Gly Gln Ser Leu		
450	455	460
Ile Ile Ile Asn Val Asn Val Ala Val Pro Ser Val His Val Pro Glu		
465	470	475
Val Pro Ser Tyr Pro Glu Thr Pro Trp Tyr Pro Asp Thr Pro Ser Tyr		
485	490	495
Pro Asp Thr Thr Ser Val Ser Ser Thr Thr Glu Leu Thr Ser Pro Val		
500	505	510
Glu Asp Tyr Thr Asp Leu Thr Thr Ile Gln Val Thr Asp Asp Arg Ser		
515	520	525
Val Trp Gly Met Thr His Ala His Ser Gly Leu Ala Ile Ala Ala Ile		
530	535	540
Val Ile Gly Ile Val Ala Leu Ala Cys Ser Leu Ala Ala Cys Val Gly		
545	550	555
Cys Cys Cys Lys Lys Arg Ser Gln Ala Val Leu Met Gln Met Lys		560
565	570	575
Ala Pro Asn Glu Cys		
580		

<210> 44
 <211> 628
 <212> PRT
 <213> Homo sapiens

<400> 44		
Met Pro Gly Ala Pro Asp Trp Ser Leu Asn Ser Ser Arg Asn Ala Arg		
1	5	10
Ser Leu Glu Gly Leu Pro Leu Cys Pro Trp Trp Ala Leu Phe Val Pro		15
20	25	30
Arg Ala Ala Ala Leu Val Gly Leu Gln Arg Lys Gln Glu Asn Ser Ser		
35	40	45
Asp Ile Phe Phe Ser Ser Pro Phe Thr Val Thr Pro Asp Ala Leu Pro		
50	55	60
Thr Ala Ile Thr Trp Glu His Ile Pro Phe Ala Lys Leu Ala Gly Leu		
65	70	75
Ile Ala Gly Pro Leu Val Glu Met Cys Arg Gln Arg Leu Ser Lys Glu		80
85	90	95
Phe Glu Ala Leu Lys Gly Glu Phe Arg Asp Leu Gly His Cys Leu Pro		
100	105	110
Gly Ala Gln Arg Gly Asn Arg Ile Thr Lys Arg Asn Lys Cys Gly Gln		

115	120	125
Ser Arg Gln Ala Leu Ile Gly Gln Arg Gln Glu Asp Ala Gly Ser Ala		
130	135	140
Pro Leu Gln Met His Pro Ser Val Ala Ala Leu Gly Ala Gly Ala Ala		
145	150	155
Leu Arg Glu Ile Gln Pro Leu Gln Arg Glu Pro Glu Leu Ser Ser Gly		
165	170	175
Pro Arg Asn Ser Arg Leu Leu Cys Trp Gly Ser Pro Ala Thr Trp Asn		
180	185	190
Pro Thr Tyr Leu Ser Arg Val Leu Gly Gln Gln Val Ala Val Thr Val		
195	200	205
Thr Glu Ala Gly Leu Gln Ala Val Pro Trp Gly Pro Ser Arg Glu Phe		
210	215	220
Asn Ala Lys Gly Ser Ser Ala Ser Ile Arg Val Gly Gln Pro Gln		
225	230	235
Lys Leu Arg Leu Arg Val Gln Arg Ser Arg Arg Gln Cys Pro Pro Val		
245	250	255
Gln Ser Ser Gln Asp Leu Pro Pro Gly Gly Ser Gln Asp Gly Asp Leu		
260	265	270
Lys Glu Pro Thr Glu Arg Val Thr Arg Asp Leu Ser Ser Gly Ala Pro		
275	280	285
Arg Gly Arg Asn Leu Pro Ala Pro Asp Gln Pro Gln Pro Pro Leu Gln		
290	295	300
Arg Gly Thr Arg Leu Arg Leu Arg Gln Arg Arg Arg Arg Leu Leu Ile		
305	310	315
Lys Lys Met Pro Ala Ala Ala Thr Ile Pro Ala Asn Ser Ser Asp Ala		
325	330	335
Pro Phe Ile Arg Pro Gly Pro Gly Thr Leu Asp Gly Arg Trp Val Ser		
340	345	350
Leu His Arg Ser Gln Gln Glu Arg Lys Arg Val Met Gln Glu Ala Cys		
355	360	365
Ala Lys Tyr Arg Ala Ser Ser Arg Arg Ala Val Thr Pro Arg His		
370	375	380
Val Ser Arg Ile Phe Val Glu Asp Arg His Arg Val Leu Tyr Cys Glu		
385	390	395
Val Pro Lys Ala Gly Cys Ser Asn Trp Lys Arg Val Leu Met Val Leu		
405	410	415
Ala Gly Leu Ala Ser Ser Thr Ala Asp Ile Gln His Asn Thr Val His		
420	425	430
Tyr Gly Ser Ala Leu Lys Arg Leu Asp Thr Phe Asp Arg Gln Gly Ile		
435	440	445
Leu His Arg Leu Ser Thr Tyr Thr Lys Met Leu Phe Val Arg Glu Pro		
450	455	460
Phe Glu Arg Leu Val Ser Ala Phe Arg Asp Lys Phe Glu His Pro Asn		
465	470	475
Ser Tyr Tyr His Pro Val Phe Gly Lys Ala Ile Leu Ala Arg Tyr Arg		
485	490	495
Ala Asn Ala Ser Arg Glu Ala Leu Arg Thr Gly Ser Gly Val Arg Phe		
500	505	510
Pro Glu Phe Val Gln Tyr Leu Leu Asp Val His Arg Pro Val Gly Met		
515	520	525
Asp Ile His Trp Asp His Val Ser Arg Leu Cys Ser Pro Cys Leu Ile		
530	535	540
Asp Tyr Asp Phe Val Gly Lys Phe Glu Ser Met Glu Asp Asp Ala Asn		
545	550	555
Phe Phe Leu Ser Leu Ile Arg Ala Pro Arg Asn Leu Thr Phe Pro Arg		
565	570	575
Phe Lys Asp Arg His Ser Gln Glu Ala Arg Thr Thr Ala Arg Ile Ala		
580	585	590

His Gln Tyr Phe Ala Gln Leu Ser Ala Leu Gln Arg Gln Arg Thr Tyr
 595 600 605
 Asp Phe Tyr Tyr Met Asp Tyr Leu Met Phe Asn Tyr Ser Lys Pro Phe
 610 615 620
 Ala Asp Leu Tyr
 625
 •
 <210> 45
 <211> 424
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Thr Leu Arg Pro Gly Thr Met Arg Leu Ala Cys Met Phe Ser Ser
 1 5 10 15
 Ile Leu Leu Phe Gly Ala Ala Gly Leu Leu Leu Phe Ile Ser Leu Gln
 20 25 30
 Asp Pro Thr Glu Leu Ala Pro Gln Gln Val Pro Gly Ile Lys Phe Asn
 35 40 45
 Ile Arg Pro Arg Gln Pro His His Asp Leu Pro Pro Gly Gly Ser Gln
 50 55 60
 Asp Gly Asp Leu Lys Glu Pro Thr Glu Arg Val Thr Arg Asp Leu Ser
 65 70 75 80
 Ser Gly Ala Pro Arg Gly Arg Asn Leu Pro Ala Pro Asp Gln Pro Gln
 85 90 95
 Pro Pro Leu Gln Arg Gly Thr Arg Leu Arg Leu Arg Gln Arg Arg Arg
 100 105 110
 Arg Leu Leu Ile Lys Lys Met Pro Ala Ala Thr Ile Pro Ala Asn
 115 120 125
 Ser Ser Asp Ala Pro Phe Ile Arg Pro Gly Pro Gly Thr Leu Asp Gly
 130 135 140
 Arg Trp Val Ser Leu His Arg Ser Gln Gln Glu Arg Lys Arg Val Met
 145 150 155 160
 Gln Glu Ala Cys Ala Lys Tyr Arg Ala Ser Ser Ser Arg Arg Ala Val
 165 170 175
 Thr Pro Arg His Val Ser Arg Ile Phe Val Glu Asp Arg His Arg Val
 180 185 190
 Leu Tyr Cys Glu Val Pro Lys Ala Gly Cys Ser Asn Trp Lys Arg Val
 195 200 205
 Leu Met Val Leu Ala Gly Leu Ala Ser Ser Thr Ala Asp Ile Gln His
 210 215 220
 Asn Thr Val His Tyr Gly Ser Ala Leu Lys Arg Leu Asp Thr Phe Asp
 225 230 235 240
 Arg Gln Gly Ile Leu His Arg Leu Ser Thr Tyr Thr Lys Met Leu Phe
 245 250 255
 Val Arg Glu Pro Phe Glu Arg Leu Val Ser Ala Phe Arg Asp Lys Phe
 260 265 270
 Glu His Pro Asn Ser Tyr Tyr His Pro Val Phe Gly Lys Ala Ile Leu
 275 280 285
 Ala Arg Tyr Arg Ala Asn Ala Ser Arg Glu Ala Leu Arg Thr Gly Ser
 290 295 300
 Gly Val Arg Phe Pro Glu Phe Val Gln Tyr Leu Leu Asp Val His Arg
 305 310 315 320
 Pro Val Gly Met Asp Ile His Trp Asp His Val Ser Arg Leu Cys Ser
 325 330 335
 Pro Cys Leu Ile Asp Tyr Asp Phe Val Gly Lys Phe Glu Ser Met Glu
 340 345 350
 Asp Asp Ala Asn Phe Phe Leu Ser Leu Ile Arg Ala Pro Arg Asn Leu
 355 360 365

Thr Phe Pro Arg Phe Lys Asp Arg His Ser Gln Glu Ala Arg Thr Thr
 370 375 380
 Ala Arg Ile Ala His Gln Tyr Phe Ala Gln Leu Ser Ala Leu Gln Arg
 385 390 395 400
 Gln Arg Thr Tyr Asp Phe Tyr Tyr Met Asp Tyr Leu Met Phe Asn Tyr
 405 410 415
 Ser Lys Pro Phe Ala Asp Leu Tyr
 420

<210> 46
 <211> 638
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Ala Gly Gly Ser Ala Thr Thr Trp Gly Tyr Pro Val Ala Leu Leu
 1 5 10 15
 Leu Leu Val Ala Thr Leu Gly Leu Gly Arg Trp Leu Gln Pro Asp Pro
 20 25 30
 Gly Leu Pro Gly Leu Arg His Ser Tyr Asp Cys Gly Ile Lys Gly Met
 35 40 45
 Gln Leu Leu Val Phe Pro Arg Pro Gly Gln Thr Leu Arg Phe Lys Val
 50 55 60
 Val Asp Glu Phe Gly Asn Arg Phe Asp Val Asn Asn Cys Ser Ile Cys
 65 70 75 80
 Tyr His Trp Val Thr Ser Arg Pro Gln Glu Pro Ala Val Phe Ser Ala
 85 90 95
 Asp Tyr Arg Gly Cys His Val Leu Glu Lys Asp Gly Arg Phe His Leu
 100 105 110
 Arg Val Phe Met Glu Ala Val Leu Pro Asn Gly Arg Val Asp Val Ala
 115 120 125
 Gln Asp Ala Thr Leu Ile Cys Pro Lys Pro Asp Pro Ser Arg Thr Leu
 130 135 140
 Asp Ser Gln Leu Ala Pro Pro Ala Met Phe Ser Val Ser Thr Pro Gln
 145 150 155 160
 Thr Leu Ser Phe Leu Pro Thr Ser Gly His Thr Ser Gln Gly Ser Gly
 165 170 175
 His Ala Phe Pro Ser Pro Leu Asp Pro Gly His Ser Ser Val His Pro
 180 185 190
 Thr Pro Ala Leu Pro Ser Pro Gly Pro Gly Pro Thr Leu Ala Thr Leu
 195 200 205
 Ala Gln Pro His Trp Gly Thr Leu Glu His Trp Asp Val Asn Lys Arg
 210 215 220
 Asp Tyr Ile Gly Thr His Leu Ser Gln Glu Gln Cys Gln Val Ala Ser
 225 230 235 240
 Gly His Leu Pro Cys Ile Val Arg Arg Thr Ser Lys Glu Ala Cys Gln
 245 250 255
 Gln Ala Gly Cys Cys Tyr Asp Asn Thr Arg Glu Val Pro Cys Tyr Tyr
 260 265 270
 Gly Asn Thr Ala Thr Val Gln Cys Phe Arg Asp Gly Tyr Phe Val Leu
 275 280 285
 Val Val Ser Gln Glu Met Ala Leu Thr His Arg Ile Thr Leu Ala Asn
 290 295 300
 Ile His Leu Ala Tyr Ala Pro Thr Ser Cys Ser Pro Thr Gln His Thr
 305 310 315 320
 Glu Ala Phe Val Val Phe Tyr Phe Pro Leu Thr His Cys Gly Thr Thr
 325 330 335
 Met Gln Val Ala Gly Asp Gln Leu Ile Tyr Glu Asn Trp Leu Val Ser
 340 345 350

Gly Ile His Ile Gln Lys Gly Pro Gln Gly Ser Ile Thr Arg Asp Ser
 355 360 365
 Thr Phe Gln Leu His Val Arg Cys Val Phe Asn Ala Ser Asp Phe Leu
 370 375 380
 Pro Ile Gln Ala Ser Ile Phe Pro Pro Pro Ser Pro Ala Pro Met Thr
 385 390 395 400
 Gln Pro Gly Pro Leu Arg Leu Glu Leu Arg Ile Ala Lys Asp Glu Thr
 405 410 415
 Phe Ser Ser Tyr Tyr Gly Glu Asp Asp Tyr Pro Ile Val Arg Leu Leu
 420 425 430
 Arg Glu Pro Val His Val Glu Val Arg Leu Leu Gln Arg Thr Asp Pro
 435 440 445
 Asn Leu Val Leu Leu His Gln Cys Trp Gly Ala Pro Ser Ala Asn
 450 455 460
 Pro Phe Gln Gln Pro Gln Trp Pro Ile Leu Ser Asp Gly Cys Pro Phe
 465 470 475 480
 Lys Gly Asp Ser Tyr Arg Thr Gln Met Val Ala Leu Asp Gly Ala Thr
 485 490 495
 Pro Phe Gln Ser His Tyr Gln Arg Phe Thr Val Ala Thr Phe Ala Leu
 500 505 510
 Leu Asp Ser Gly Ser Gln Arg Ala Leu Arg Gly Leu Val Tyr Leu Phe
 515 520 525
 Cys Ser Thr Ser Ala Cys His Thr Ser Gly Leu Glu Thr Cys Ser Thr
 530 535 540
 Ala Cys Ser Thr Gly Thr Arg Gln Arg Arg Ser Ser Gly His Arg
 545 550 555 560
 Asn Asp Thr Ala Arg Pro Gln Asp Ile Val Ser Ser Pro Gly Pro Val
 565 570 575
 Gly Phe Glu Asp Ser Tyr Gly Gln Glu Pro Thr Leu Gly Pro Thr Asp
 580 585 590
 Ser Asn Gly Asn Ser Ser Leu Arg Pro Leu Leu Trp Ala Val Leu Leu
 595 600 605
 Leu Pro Ala Val Ala Leu Val Leu Gly Phe Gly Val Phe Val Gly Leu
 610 615 620
 Ser Gln Thr Trp Ala Gln Lys Leu Trp Glu Ser Asn Arg Gln
 625 630 635

<210> 47
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 47

Met Lys Pro Leu Ala Gln Leu Leu Leu Phe Leu Leu Gln Phe Gln Lys
 1 5 10 15
 Gly Asn Leu Val Ser Gln Ser Ser Ser Thr Pro Leu Met Val Asn Gly
 20 25 30
 Val Leu Gly Glu Ser Val Thr Leu Pro Leu Glu Phe Pro Ala Gly Glu
 35 40 45
 Arg Ile Gln Phe Ile Thr Trp Leu Cys Asn Gly Thr Ser Phe Ala Phe
 50 55 60
 Leu Glu Pro Tyr Glu Gly Lys Ser Pro Lys Ile Tyr Val Thr His Pro
 65 70 75 80
 Lys Trp Gln Lys Arg Leu Ser Phe Thr Gln Ser Tyr Ser Pro Gln Leu
 85 90 95
 Ser Asn Leu Glu Met Glu Asn Ile Gly Phe Tyr Ser Ala Gln Ile Ala
 100 105 110
 Thr Glu Thr Ser Ala Lys Leu Ser Ser Tyr Thr Leu Arg Ile Phe Lys
 115 120 125

Gln Leu Pro Arg Pro Gln Val Arg Val Asp Ser Ile Ile Ser Glu Asn
 130 135 140
 Gly Ile Cys Asn Ala Ile Leu Arg Cys Ser Val Glu Glu Gly Gly Glu
 145 150 155 160
 Thr Ile Thr Tyr Glu Trp Thr Ser Met Gly Pro Gly Ala Ala Val Ser
 165 170 175
 His Val Gly Leu His Asp Leu Asp Trp Ile Tyr Thr Cys Thr Ala Leu
 180 185 190
 Asn Pro Val Ser Tyr Ser Asn Ser Thr Leu Thr Leu Ala Ala Gln Leu
 195 200 205
 Cys Ala Ser Lys Ser Pro Leu Leu Val Ser Leu Ala Pro Leu Gly Asn
 210 215 220
 Val Leu Ser Gly Leu
 225

<210> 48
 <211> 310
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met Lys Pro Leu Ala Gln Leu Leu Leu Phe Leu Leu Gln Phe Gln Lys
 1 5 10 15
 Gly Asn Leu Val Ser Gln Ser Ser Ser Thr Pro Leu Met Val Asn Gly
 20 25 30
 Val Leu Gly Glu Ser Val Thr Leu Pro Leu Glu Phe Pro Ala Gly Glu
 35 40 45
 Arg Ile Gln Phe Ile Thr Trp Leu Cys Asn Gly Thr Ser Phe Ala Phe
 50 55 60
 Leu Glu Pro Tyr Glu Gly Lys Ser Pro Lys Ile Tyr Val Thr His Pro
 65 70 75 80
 Lys Trp Gln Lys Arg Leu Ser Phe Thr Gln Ser Tyr Ser Pro Gln Leu
 85 90 95
 Ser Asn Leu Glu Met Glu Asn Ile Gly Phe Tyr Ser Ala Gln Ile Ala
 100 105 110
 Thr Glu Thr Ser Ala Lys Leu Ser Ser Tyr Thr Leu Arg Ile Phe Lys
 115 120 125
 Gln Leu Pro Arg Pro Gln Val Arg Val Asp Ser Ile Ile Ser Glu Asn
 130 135 140
 Gly Ile Cys Asn Ala Ile Leu Arg Cys Ser Val Glu Glu Gly Gly Glu
 145 150 155 160
 Thr Ile Thr Tyr Glu Trp Thr Ser Met Gly Pro Gly Ala Ala Val Ser
 165 170 175
 His Val Gly Leu His Asp Leu Asp Trp Ile Tyr Thr Cys Thr Ala Leu
 180 185 190
 Asn Pro Val Ser Tyr Ser Asn Ser Thr Leu Thr Leu Ala Ala Gln Leu
 195 200 205
 Cys Ala Ser Ser Lys Ala Ala Glu Gly Thr Tyr Cys Pro Val Lys Trp
 210 215 220
 Ile Phe Leu Gly Asn Arg Leu Leu Leu Val Phe Leu Gly Val Leu
 225 230 235 240
 Arg Thr Trp His Ile Gln Ala Gln Val Leu Ser Lys Pro Leu Arg Pro
 245 250 255
 Asn Ser Gly Glu Leu Val Asn Leu Ser Ser Ile Pro Tyr Pro Trp Glu
 260 265 270
 Pro Ser His Thr Ala Asp Ala Thr Trp Leu Gly Lys Trp Gly Gly Ser
 275 280 285
 Glu Gly Glu Arg Lys Ser Thr Trp Asn Ile Ser Thr Thr Lys Arg His
 290 295 300

Trp Lys Ser Phe Tyr Lys
305 310

<210> 49
<211> 841
<212> PRT
<213> Homo sapiens

<400> 49
Met Lys Leu Trp Ile His Leu Phe Tyr Ser Ser Leu Leu Ala Cys Ile
1 5 10 15
Ser Leu His Ser Gln Thr Pro Val Leu Ser Ser Arg Gly Ser Cys Asp
20 25 30
Ser Leu Cys Asn Cys Glu Glu Lys Asp Gly Thr Met Leu Ile Asn Cys
35 40 45
Glu Ala Lys Gly Ile Lys Met Val Ser Glu Ile Ser Val Pro Pro Ser
50 55 60
Arg Pro Phe Gln Leu Ser Leu Leu Asn Asn Gly Leu Thr Met Leu His
65 70 75 80
Thr Asn Asp Phe Ser Gly Leu Thr Asn Ala Ile Ser Ile His Leu Gly
85 90 95
Phe Asn Asn Ile Ala Asp Ile Glu Ile Gly Ala Phe Asn Gly Leu Gly
100 105 110
Leu Leu Lys Gln Leu His Ile Asn His Asn Ser Leu Glu Ile Leu Lys
115 120 125
Glu Asp Thr Phe His Gly Leu Glu Asn Leu Glu Phe Leu Gln Ala Asp
130 135 140
Asn Asn Phe Ile Thr Val Ile Glu Pro Ser Ala Phe Ser Lys Leu Asn
145 150 155 160
Arg Leu Lys Val Leu Ile Leu Asn Asp Asn Ala Ile Glu Ser Leu Pro
165 170 175
Pro Asn Ile Phe Arg Phe Val Pro Leu Thr His Leu Asp Leu Arg Gly
180 185 190
Asn Gln Leu Gln Thr Leu Pro Tyr Val Gly Phe Leu Glu His Ile Gly
195 200 205
Arg Ile Leu Asp Leu Gln Leu Glu Asp Asn Lys Trp Ala Cys Asn Cys
210 215 220
Asp Leu Leu Gln Leu Lys Thr Trp Leu Glu Asn Met Pro Pro Gln Ser
225 230 235 240
Ile Ile Gly Asp Val Val Cys Asn Ser Pro Pro Phe Phe Lys Gly Ser
245 250 255
Ile Leu Ser Arg Leu Lys Lys Glu Ser Ile Cys Pro Thr Pro Pro Val
260 265 270
Tyr Glu Glu His Glu Asp Pro Ser Gly Ser Leu His Leu Ala Ala Thr
275 280 285
Ser Ser Ile Asn Asp Ser Arg Met Ser Thr Lys Thr Thr Ser Ile Leu
290 295 300
Lys Leu Pro Thr Lys Ala Pro Gly Leu Ile Pro Tyr Ile Thr Lys Pro
305 310 315 320
Ser Thr Gln Leu Pro Gly Pro Tyr Cys Pro Ile Pro Cys Asn Cys Lys
325 330 335
Val Leu Ser Pro Ser Gly Leu Leu Ile His Cys Gln Glu Arg Asn Ile
340 345 350
Glu Ser Leu Ser Asp Leu Arg Pro Pro Pro Gln Asn Pro Arg Lys Leu
355 360 365
Ile Leu Ala Gly Asn Ile Ile His Ser Leu Met Lys Ser Asp Leu Val
370 375 380
Glu Tyr Phe Thr Leu Glu Met Leu His Leu Gly Asn Asn Arg Ile Glu
385 390 395 400

Val Leu Glu Glu Gly Ser Phe Met Asn Leu Thr Arg Leu Gln Lys Leu
 405 410 415
 Tyr Leu Asn Gly Asn His Leu Thr Lys Leu Ser Lys Gly Met Phe Leu
 420 425 430
 Gly Leu His Asn Leu Glu Tyr Leu Tyr Leu Glu Tyr Asn Ala Ile Lys
 435 440 445
 Glu Ile Leu Pro Gly Thr Phe Asn Pro Met Pro Lys Leu Lys Val Leu
 450 455 460
 Tyr Leu Asn Asn Asn Leu Leu Gln Val Leu Pro Pro His Ile Phe Ser
 465 470 475 480
 Gly Val Pro Leu Thr Lys Val Asn Leu Lys Thr Asn Gln Phe Thr His
 485 490 495
 Leu Pro Val Ser Asn Ile Leu Asp Asp Leu Asp Leu Leu Thr Gln Ile
 500 505 510
 Asp Leu Glu Asp Asn Pro Trp Asp Cys Ser Cys Asp Leu Val Gly Leu
 515 520 525
 Gln Gln Trp Ile Gln Lys Leu Ser Lys Asn Thr Val Thr Asp Asp Ile
 530 535 540
 Leu Cys Thr Ser Pro Gly His Leu Asp Lys Lys Glu Leu Lys Ala Leu
 545 550 555 560
 Asn Ser Glu Ile Leu Cys Pro Gly Leu Val Asn Asn Pro Ser Met Pro
 565 570 575
 Thr Gln Thr Ser Tyr Leu Met Val Thr Thr Pro Ala Thr Thr Asn
 580 585 590
 Thr Ala Asp Thr Ile Leu Arg Ser Leu Thr Asp Ala Val Pro Leu Ser
 595 600 605
 Val Leu Ile Leu Gly Leu Leu Ile Met Phe Ile Thr Ile Val Phe Cys
 610 615 620
 Ala Ala Gly Ile Val Val Leu Val Leu His Arg Arg Arg Arg Tyr Lys
 625 630 635 640
 Lys Lys Gln Val Asp Glu Gln Met Arg Asp Asn Ser Pro Val His Leu
 645 650 655
 Gln Tyr Ser Met Tyr Gly His Lys Thr Thr His His Thr Thr Glu Arg
 660 665 670
 Pro Ser Ala Ser Leu Tyr Glu Gln His Met Val Ser Pro Met Val His
 675 680 685
 Val Tyr Arg Ser Pro Ser Phe Gly Pro Lys His Leu Glu Glu Glu
 690 695 700
 Glu Arg Asn Glu Lys Glu Gly Ser Asp Ala Lys His Leu Gln Arg Ser
 705 710 715 720
 Leu Leu Glu Gln Glu Asn His Ser Pro Leu Thr Gly Ser Asn Met Lys
 725 730 735
 Tyr Lys Thr Thr Asn Gln Ser Thr Glu Phe Leu Ser Phe Gln Asp Ala
 740 745 750
 Ser Ser Leu Tyr Arg Asn Ile Leu Glu Lys Glu Arg Glu Leu Gln Gln
 755 760 765
 Leu Gly Ile Thr Glu Tyr Leu Arg Lys Asn Ile Ala Gln Leu Gln Pro
 770 775 780
 Asp Met Glu Ala His Tyr Pro Gly Ala His Glu Glu Leu Lys Leu Met
 785 790 795 800
 Glu Thr Leu Met Tyr Ser Arg Pro Arg Lys Val Leu Val Glu Gln Thr
 805 810 815
 Lys Asn Glu Tyr Phe Glu Leu Lys Ala Asn Leu His Ala Glu Pro Asp
 820 825 830
 Tyr Leu Glu Val Leu Glu Gln Gln Thr
 835 840

<210> 50

<211> 241

<212> PRT
 <213> Homo sapiens

<400> 50

Met	Gly	Asn	Pro	Gly	Leu	Ala	Trp	Leu	Val	Leu	Leu	Gly	Leu	Val	Leu
1				5					10					15	
Leu	Leu	Ser	Ser	Phe	Met	Glu	Arg	Gly	Gly	His	Ser	Pro	Ser	Pro	Ala
				20				25					30		
Ala	Leu	Ser	Ala	Met	Glu	Asn	Leu	Ile	Thr	Tyr	Ala	Val	Gln	Lys	Gly
				35				40				45			
His	Leu	Ser	Ser	Ser	Tyr	Val	Gln	Pro	Leu	Leu	Val	Lys	Gly	Glu	Asn
				50				55			60				
Cys	Leu	Ala	Pro	Arg	Gln	Lys	Thr	Ser	Leu	Lys	Lys	Ala	Cys	Pro	Gly
				65				70		75			80		
Val	Val	Pro	Arg	Ser	Val	Trp	Gly	Ala	Arg	Glu	Thr	His	Cys	Pro	Arg
					85				90			95			
Met	Thr	Leu	Pro	Ala	Lys	Tyr	Gly	Ile	Ile	Ile	His	Thr	Ala	Gly	Arg
				100				105			110				
Thr	Cys	Asn	Ile	Ser	Asp	Glu	Cys	Arg	Leu	Leu	Val	Arg	Asp	Ile	Gln
				115				120			125				
Ser	Phe	Tyr	Ile	Asp	Arg	Leu	Lys	Ser	Cys	Asp	Ile	Gly	Tyr	Asn	Phe
	130					135					140				
Leu	Val	Gly	Gln	Asp	Gly	Ala	Ile	Tyr	Glu	Gly	Val	Gly	Trp	Asn	Val
	145					150				155			160		
Gln	Gly	Ser	Ser	Thr	Pro	Gly	Tyr	Asp	Asp	Ile	Ala	Leu	Gly	Ile	Thr
				165				170			175				
Phe	Met	Gly	Thr	Phe	Thr	Gly	Ile	Pro	Pro	Asn	Ala	Ala	Leu	Glu	
				180				185			190				
Ala	Ala	Gln	Asp	Leu	Ile	Gln	Cys	Ala	Met	Val	Lys	Gly	Tyr	Leu	Thr
				195				200			205				
Pro	Asn	Tyr	Leu	Leu	Val	Gly	His	Ser	Asp	Val	Ala	Arg	Thr	Leu	Ser
	210					215					220				
Pro	Gly	Gln	Ala	Leu	Tyr	Asn	Ile	Ile	Ser	Thr	Trp	Pro	His	Phe	Lys
	225					230				235			240		
His															

<210> 51
 <211> 369
 <212> PRT
 <213> Homo sapiens

<400> 51

Met	Leu	Pro	Trp	Leu	Leu	Val	Phe	Ser	Ala	Leu	Gly	Leu	Gln	Ala	Trp
1				5					10				15		
Gly	Asp	Ser	Ser	Trp	Asn	Lys	Thr	Gln	Ala	Lys	Gln	Val	Ser	Glu	Gly
				20				25			30				
Leu	Gln	Tyr	Leu	Phe	Glu	Asn	Ile	Ser	Gln	Leu	Thr	Glu	Lys	Asp	Val
				35				40			45				
Ser	Thr	Thr	Val	Ser	Arg	Lys	Ala	Trp	Gly	Ala	Glu	Ala	Val	Gly	Cys
				50				55			60				
Ser	Ile	Gln	Leu	Thr	Thr	Pro	Val	Asn	Val	Leu	Val	Ile	His	His	Val
	65				70				75			80			
Pro	Gly	Leu	Glu	Cys	His	Asp	Arg	Thr	Val	Cys	Ser	Gln	Arg	Leu	Arg
				85				90			95				
Glu	Leu	Gln	Ala	His	His	Val	His	Asn	Asn	Ser	Gly	Cys	Asp	Val	Ala
				100				105			110				
Tyr	Asn	Phe	Leu	Val	Gly	Asp	Asp	Gly	Arg	Val	Tyr	Glu	Gly	Val	Gly
				115				120			125				

Trp Asn Ile Gln Gly Val His Thr Gln Gly Tyr Asn Asn Ile Ser Leu
 130 135 140
 Gly Phe Ala Phe Phe Gly Thr Lys Lys Gly His Ser Pro Ser Pro Ala
 145 150 155 160
 Ala Leu Ser Ala Met Glu Asn Leu Ile Thr Tyr Ala Val Gln Lys Gly
 165 170 175
 His Leu Ser Ser Ser Tyr Val Gln Pro Leu Leu Val Lys Gly Glu Asn
 180 185 190
 Cys Leu Ala Pro Arg Gln Lys Thr Ser Leu Lys Lys Ala Cys Pro Gly
 195 200 205
 Val Val Pro Arg Ser Val Trp Gly Ala Arg Glu Thr His Cys Pro Arg
 210 215 220
 Met Thr Leu Pro Ala Lys Tyr Gly Ile Ile Ile His Thr Ala Gly Arg
 225 230 235 240
 Thr Cys Asn Ile Ser Asp Glu Cys Arg Leu Leu Val Arg Asp Ile Gln
 245 250 255
 Ser Phe Tyr Ile Asp Arg Leu Lys Ser Cys Asp Ile Gly Tyr Asn Phe
 260 265 270
 Leu Val Gly Gln Asp Gly Ala Ile Tyr Glu Gly Val Gly Trp Asn Val
 275 280 285
 Gln Gly Ser Ser Thr Pro Gly Tyr Asp Asp Ile Ala Leu Gly Ile Thr
 290 295 300
 Phe Met Gly Thr Phe Thr Gly Ile Pro Pro Asn Ala Ala Leu Glu
 305 310 315 320
 Ala Ala Gln Asp Leu Ile Gln Cys Ala Met Val Lys Gly Tyr Leu Thr
 325 330 335
 Pro Asn Tyr Leu Leu Val Gly His Ser Asp Val Ala Arg Thr Leu Ser
 340 345 350
 Pro Gly Gln Ala Leu Tyr Asn Ile Ile Ser Thr Trp Pro His Phe Lys
 355 360 365
 His

<210> 52
 <211> 382
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Ala Pro Arg Ala Gly Gln Pro Gly Leu Gln Gly Leu Leu Val
 1 5 10 15
 Ala Ala Ala Leu Ser Gln Pro Ala Ala Pro Cys Pro Phe Gln Cys Tyr
 20 25 30
 Cys Phe Gly Gly Pro Lys Leu Leu Leu Arg Cys Ala Ser Gly Ala Glu
 35 40 45
 Leu Arg Gln Pro Pro Arg Asp Val Pro Pro Asp Ala Arg Asn Leu Thr
 50 55 60
 Ile Val Gly Ala Asn Leu Thr Val Leu Arg Ala Ala Ala Phe Ala Gly
 65 70 75 80
 Gly Asp Gly Asp Gly Asp Gln Ala Ala Gly Val Arg Leu Pro Leu Leu
 85 90 95
 Ser Ala Leu Arg Leu Thr His Asn His Ile Glu Val Val Glu Asp Gly
 100 105 110
 Ala Phe Asp Gly Leu Pro Ser Leu Ala Ala Leu Asp Leu Ser His Asn
 115 120 125
 Pro Leu Arg Ala Leu Gly Gly Ala Phe Arg Gly Leu Pro Ala Leu
 130 135 140
 Arg Ser Leu Gln Leu Asn His Ala Leu Val Arg Gly Gly Pro Ala Leu
 145 150 155 160

Leu Ala Ala Leu Asp Ala Ala Leu Ala Pro Leu Ala Glu Leu Arg Leu
 165 170 175
 Leu Gly Leu Ala Gly Asn Ala Leu Ser Arg Leu Pro Pro Ala Ala Leu
 180 185 190
 Arg Leu Ala Arg Leu Glu Gln Leu Asp Val Arg Leu Asn Ala Leu Ala
 195 200 205
 Gly Leu Asp Pro Asp Glu Leu Arg Ala Leu Glu Arg Asp Gly Gly Leu
 210 215 220
 Pro Gly Pro Arg Leu Leu Ala Asp Asn Pro Leu Arg Cys Gly Cys
 225 230 235 240
 Ala Ala Arg Pro Leu Leu Ala Trp Leu Arg Asn Ala Thr Glu Arg Val
 245 250 255
 Pro Asp Ser Arg Arg Leu Arg Cys Ala Ala Pro Arg Ala Leu Leu Asp
 260 265 270
 Arg Pro Leu Leu Asp Leu Asp Gly Ala Arg Leu Arg Cys Ala Asp Ser
 275 280 285
 Gly Ala Asp Ala Arg Gly Glu Ala Glu Ala Ala Gly Pro Glu Leu
 290 295 300
 Glu Ala Ser Tyr Val Phe Phe Gly Leu Val Leu Ala Leu Ile Gly Leu
 305 310 315 320
 Ile Phe Leu Met Val Leu Tyr Leu Asn Arg Arg Gly Ile Gln Arg Trp
 325 330 335
 Met Arg Asn Leu Arg Glu Ala Cys Arg Asp Gln Met Glu Gly Tyr His
 340 345 350
 Tyr Arg Tyr Glu Gln Asp Ala Asp Pro Arg Arg Ala Pro Ala Pro Ala
 355 360 365
 Ala Pro Ala Gly Ser Arg Ala Thr Ser Pro Gly Ser Gly Leu
 370 375 380

<210> 53
 <211> 185
 <212> PRT
 <213> Homo sapiens

<400> 53

Met Met Leu Leu Leu Cys Leu Gly Leu Thr Leu Val Cys Ala Gln
 1 5 10 15
 Glu Glu Glu Asn Asn Asp Ala Val Thr Ser Asn Phe Asp Leu Ser Lys
 20 25 30
 Ile Ser Gly Glu Trp Tyr Ser Val Leu Leu Ala Ser Asp Cys Arg Glu
 35 40 45
 Lys Ile Glu Glu Asp Gly Ser Met Arg Val Phe Val Lys His Ile Asp
 50 55 60
 Tyr Leu Gly Asn Ser Ser Leu Thr Phe Lys Leu His Glu Ile Glu Asn
 65 70 75 80
 Gly Asn Cys Thr Glu Ile Asn Leu Ala Cys Lys Pro Thr Glu Lys Asn
 85 90 95
 Ala Ile Cys Ser Thr Asp Tyr Asn Gly Leu Asn Val Ile Asp Ile Leu
 100 105 110
 Glu Thr Asp Tyr Asp Asn Tyr Ile Tyr Phe Tyr Asn Lys Asn Ile Lys
 115 120 125
 Asn Gly Glu Thr Phe Leu Met Leu Glu Leu Tyr Val Arg Thr Pro Asp
 130 135 140
 Val Ser Ser Gln Leu Lys Glu Arg Phe Val Lys Tyr Cys Glu Glu His
 145 150 155 160
 Gly Ile Asp Lys Glu Asn Ile Phe Asp Leu Thr Lys Val Asp Arg Cys
 165 170 175
 Leu Gln Ala Arg Asp Glu Gly Ala Ala
 180 185

<210> 54
<211> 586
<212> PRT
<213> Homo sapiens

<400> 54
Met His Tyr Asn Leu Gln Gly Pro Thr Arg Arg Ile Arg Ile Ser Leu
1 5 10 15
Leu Asn Asp Gly Gly Leu Lys Ile Ala Asn Val Thr Lys Ala Asp Ala
20 25 30
Gly Thr Tyr Thr Cys Met Ala Glu Asn Gln Phe Gly Lys Ala Asn Gly
35 40 45
Thr Thr His Leu Val Val Thr Glu Pro Thr Arg Ile Thr Leu Ala Pro
50 55 60
Ser Asn Met Asp Val Ser Val Gly Glu Ser Val Ile Leu Pro Cys Gln
65 70 75 80
Val Gln His Asp Pro Leu Leu Asp Ile Ile Phe Thr Trp Tyr Phe Asn
85 90 95
Gly Ala Leu Ala Asp Phe Lys Lys Asp Gly Ser His Phe Glu Lys Val
100 105 110
Gly Gly Ser Ser Ser Gly Asp Leu Met Ile Arg Asn Ile Gln Leu Lys
115 120 125
His Ser Gly Lys Tyr Val Cys Met Val Gln Thr Gly Val Asp Ser Val
130 135 140
Ser Ser Ala Ala Asp Leu Ile Val Arg Gly Ser Pro Gly Pro Pro Glu
145 150 155 160
Asn Val Lys Val Asp Glu Ile Thr Asp Thr Thr Ala Gln Leu Ser Trp
165 170 175
Lys Glu Gly Lys Asp Asn His Ser Pro Val Ile Ser Tyr Ser Ile Gln
180 185 190
Ala Arg Thr Pro Phe Ser Val Gly Trp Gln Thr Val Thr Thr Val Pro
195 200 205
Glu Val Ile Asp Gly Lys Thr His Thr Ala Thr Val Val Glu Leu Asn
210 215 220
Pro Trp Val Glu Tyr Glu Phe Arg Val Val Ala Ser Asn Lys Ile Gly
225 230 235 240
Gly Gly Glu Pro Ser Leu Pro Ser Glu Lys Val Arg Thr Glu Glu Ala
245 250 255
Val Pro Glu Val Pro Pro Ser Glu Val Asn Gly Gly Gly Ser Arg
260 265 270
Ser Glu Leu Val Ile Thr Trp Asp Pro Val Pro Glu Glu Leu Gln Asn
275 280 285
Gly Glu Gly Phe Gly Tyr Val Val Ala Phe Arg Pro Leu Gly Val Thr
290 295 300
Thr Trp Ile Gln Thr Val Val Thr Ser Pro Asp Thr Pro Arg Tyr Val
305 310 315 320
Phe Arg Asn Glu Ser Ile Val Pro Tyr Ser Pro Tyr Glu Val Lys Val
325 330 335
Gly Val Tyr Asn Asn Lys Gly Glu Gly Pro Phe Ser Pro Val Thr Thr
340 345 350
Val Phe Ser Ala Glu Glu Glu Pro Thr Val Ala Pro Ser Gln Val Ser
355 360 365
Ala Asn Ser Leu Ser Ser Ser Glu Ile Glu Val Ser Trp Asn Thr Ile
370 375 380
Pro Trp Lys Leu Ser Asn Gly His Leu Leu Gly Tyr Glu Val Arg Tyr
385 390 395 400
Trp Asn Gly Gly Lys Glu Glu Ser Ser Lys Met Lys Val Ala
405 410 415

Gly Asn Glu Thr Ser Ala Arg Leu Arg Gly Leu Lys Ser Asn Leu Ala
 420 425 430
 Tyr Tyr Thr Ala Val Arg Ala Tyr Asn Ser Ala Gly Ala Gly Pro Phe
 435 440 445
 Ser Ala Thr Val Asn Val Thr Thr Lys Lys Thr Pro Pro Ser Gln Pro
 450 455 460
 Pro Gly Asn Val Val Trp Asn Ala Thr Asp Thr Lys Val Leu Leu Asn
 465 470 475 480
 Trp Glu Gln Val Lys Ala Met Glu Asn Glu Ser Glu Val Thr Gly Tyr
 485 490 495
 Lys Val Phe Tyr Arg Thr Ser Ser Gln Asn Asn Val Gln Val Leu Asn
 500 505 510
 Thr Asn Lys Thr Ser Ala Glu Leu Val Leu Pro Ile Lys Glu Asp Tyr
 515 520 525
 Ile Ile Glu Val Lys Ala Thr Thr Asp Gly Gly Asp Gly Thr Ser Ser
 530 535 540
 Glu Gln Ile Arg Ile Pro Arg Ile Thr Ser Met Asp Ala Arg Gly Ser
 545 550 555 560
 Thr Ser Ala Ile Ser Asn Val His Pro Met Ser Ser Tyr Met Pro Ile
 565 570 575
 Val Leu Phe Leu Ile Val Tyr Val Leu Trp
 580 585

<210> 55
 <211> 1026
 <212> PRT
 <213> Homo sapiens

<400> 55
 Met Leu Val Val Glu Arg Val Met Val Leu Pro Ile Gly Phe Pro Leu
 1 5 10 15
 Gly Val Ser Asp Asp Ser Thr Leu His Gly Pro Ile Phe Ile Gln Glu
 20 25 30
 Pro Ser Pro Val Met Phe Pro Leu Asp Ser Glu Glu Lys Lys Val Lys
 35 40 45
 Leu Asn Cys Glu Val Lys Gly Asn Pro Lys Pro His Ile Arg Trp Lys
 50 55 60
 Leu Asn Gly Thr Asp Val Asp Thr Gly Met Asp Phe Arg Tyr Ser Val
 65 70 75 80
 Val Glu Gly Ser Leu Leu Ile Asn Asn Pro Asn Lys Thr Gln Asp Ala
 85 90 95
 Gly Thr Tyr Gln Cys Thr Ala Thr Asn Ser Phe Gly Thr Ile Val Ser
 100 105 110
 Arg Glu Ala Lys Leu Gln Phe Ala Tyr Leu Asp Asn Phe Lys Thr Arg
 115 120 125
 Thr Arg Ser Thr Val Ser Val Arg Arg Gly Gln Gly Met Val Leu Leu
 130 135 140
 Cys Gly Pro Pro Pro His Ser Gly Glu Leu Ser Tyr Ala Trp Ile Phe
 145 150 155 160
 Asn Glu Tyr Pro Ser Tyr Gln Asp Asn Arg Arg Phe Val Ser Gln Glu
 165 170 175
 Thr Gly Asn Leu Tyr Ile Ala Lys Val Glu Lys Ser Asp Val Gly Asn
 180 185 190
 Tyr Thr Cys Val Val Thr Asn Thr Val Thr Asn His Lys Val Leu Gly
 195 200 205
 Pro Pro Thr Pro Leu Ile Leu Arg Asn Asp Gly Val Met Gly Glu Tyr
 210 215 220
 Glu Pro Lys Ile Glu Val Gln Phe Pro Glu Thr Val Pro Thr Ala Lys
 225 230 235 240

Gly Ala Thr Val Lys Leu Glu Cys Phe Ala Leu Gly Asn Pro Val Pro
 245 250 255
 Thr Ile Ile Trp Arg Arg Ala Asp Gly Lys Pro Ile Ala Arg Lys Ala
 260 265 270
 Arg Arg His Lys Ser Asn Gly Ile Leu Glu Ile Pro Asn Phe Gln Gln
 275 280 285
 Glu Asp Ala Gly Leu Tyr Glu Cys Val Ala Glu Asn Ser Arg Gly Lys
 290 295 300
 Asn Val Ala Arg Gly Gln Leu Thr Phe Tyr Ala Gln Pro Asn Trp Ile
 305 310 315 320
 Gln Lys Ile Asn Asp Ile His Val Ala Met Glu Glu Asn Val Phe Trp
 325 330 335
 Glu Cys Lys Ala Asn Gly Arg Pro Lys Pro Thr Tyr Lys Trp Leu Lys
 340 345 350
 Asn Gly Glu Pro Leu Leu Thr Arg Asp Arg Ile Gln Ile Glu Gln Gly
 355 360 365
 Thr Leu Asn Ile Thr Ile Val Asn Leu Ser Asp Ala Gly Met Tyr Gln
 370 375 380
 Cys Leu Ala Glu Asn Lys His Gly Val Ile Phe Ser Asn Ala Glu Leu
 385 390 395 400
 Ser Val Ile Ala Val Gly Pro Asp Phe Ser Arg Thr Leu Leu Lys Arg
 405 410 415
 Val Thr Leu Val Lys Val Gly Gly Glu Val Val Ile Glu Cys Lys Pro
 420 425 430
 Lys Ala Ser Pro Lys Pro Val Tyr Thr Trp Lys Lys Gly Arg Asp Ile
 435 440 445
 Leu Lys Glu Asn Glu Arg Ile Thr Ile Ser Glu Asp Gly Asn Leu Arg
 450 455 460
 Ile Ile Asn Val Thr Lys Ser Asp Ala Gly Ser Tyr Thr Cys Ile Ala
 465 470 475 480
 Thr Asn His Phe Gly Thr Ala Ser Ser Thr Gly Asn Leu Val Val Lys
 485 490 495
 Asp Pro Thr Arg Val Met Val Pro Pro Ser Ser Met Asp Val Thr Val
 500 505 510
 Gly Glu Ser Ile Val Leu Pro Cys Gln Val Thr His Asp His Ser Leu
 515 520 525
 Asp Ile Val Phe Thr Trp Ser Phe Asn Gly His Leu Ile Asp Phe Asp
 530 535 540
 Arg Asp Gly Asp His Phe Glu Arg Val Gly Gly Asp Ser Ala Gly Asp
 545 550 555 560
 Leu Met Ile Arg Asn Ile Gln Leu Lys His Ala Gly Lys Tyr Val Cys
 565 570 575
 Met Val Gln Thr Ser Val Asp Arg Leu Ser Ala Ala Ala Asp Leu Ile
 580 585 590
 Val Arg Gly Pro Pro Gly Pro Pro Glu Ala Val Thr Ile Asp Glu Ile
 595 600 605
 Thr Asp Thr Thr Ala Gln Leu Ser Trp Arg Pro Gly Pro Asp Asn His
 610 615 620
 Ser Pro Ile Thr Met Tyr Val Ile Gln Ala Arg Thr Pro Phe Ser Val
 625 630 635 640
 Gly Trp Gln Ala Val Ser Thr Val Pro Glu Leu Ile Asp Gly Lys Thr
 645 650 655
 Phe Thr Ala Thr Val Val Gly Leu Asn Pro Trp Val Glu Tyr Glu Phe
 660 665 670
 Arg Thr Val Ala Ala Asn Val Ile Gly Ile Gly Glu Pro Ser Arg Pro
 675 680 685
 Ser Glu Lys Arg Arg Thr Glu Glu Ala Leu Pro Glu Val Thr Pro Ala
 690 695 700
 Asn Val Ser Gly Gly Ser Lys Ser Glu Leu Val Ile Thr Trp

705 710 715 720
 Glu Thr Val Pro Glu Glu Leu Gln Asn Gly Arg Gly Phe Gly Tyr Val
 725 730 735
 Val Ala Phe Arg Pro Tyr Gly Lys Met Ile Trp Met Leu Thr Val Leu
 740 745 750
 Ala Ser Ala Asp Ala Ser Arg Tyr Val Phe Arg Asn Glu Ser Val His
 755 760 765
 Pro Phe Ser Pro Phe Glu Val Lys Val Gly Val Phe Asn Asn Lys Gly
 770 775 780
 Glu Gly Pro Phe Ser Pro Thr Thr Val Val Tyr Ser Ala Glu Glu Glu
 785 790 795 800
 Pro Thr Lys Pro Pro Ala Ser Ile Phe Ala Arg Ser Leu Ser Ala Thr
 805 810 815
 Asp Ile Glu Val Phe Trp Ala Ser Pro Leu Glu Lys Asn Arg Gly Arg
 820 825 830
 Ile Gln Gly Tyr Glu Val Lys Tyr Trp Arg His Glu Asp Lys Glu Glu
 835 840 845
 Asn Ala Arg Lys Ile Arg Thr Val Gly Asn Gln Thr Ser Thr Lys Ile
 850 855 860
 Thr Asn Leu Lys Gly Ser Val Leu Tyr His Leu Ala Val Lys Ala Tyr
 865 870 875 880
 Asn Ser Ala Gly Thr Gly Pro Ser Ser Ala Thr Val Asn Val Thr Thr
 885 890 895
 Arg Lys Pro Pro Pro Ser Gln Pro Pro Gly Asn Ile Ile Trp Asn Ser
 900 905 910
 Ser Asp Ser Lys Ile Ile Leu Asn Trp Asp Gln Val Lys Ala Leu Asp
 915 920 925
 Asn Glu Ser Glu Val Lys Gly Tyr Lys Val Leu Tyr Arg Trp Asn Arg
 930 935 940
 Gln Ser Ser Thr Ser Val Ile Glu Thr Asn Lys Thr Ser Val Glu Leu
 945 950 955 960
 Ser Leu Pro Phe Asp Glu Asp Tyr Ile Ile Glu Ile Lys Pro Phe Ser
 965 970 975
 Asp Gly Gly Asp Gly Ser Ser Ser Glu Gln Ile Arg Ile Pro Lys Ile
 980 985 990
 Ser Asn Ala Tyr Ala Arg Gly Ser Gly Ala Ser Thr Ser Asn Ala Cys
 995 1000 1005
 Thr Leu Ser Ala Ile Ser Thr Ile Met Ile Ser Leu Thr Ala Arg Ser
 1010 1015 1020
 Ser Leu
 1025

<210> 56
 <211> 844
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Asp Asn Pro Gln Ala Leu Pro Leu Phe Leu Leu Ala Ser Leu
 1 5 10 15
 Val Gly Ile Leu Thr Leu Arg Ala Ser Ser Gly Leu Gln Gln Thr Asn
 20 25 30
 Phe Ser Ser Ala Phe Ser Ser Asp Ser Lys Ser Ser Ser Gln Gly Leu
 35 40 45
 Gly Val Glu Val Pro Ser Ile Lys Pro Pro Ser Trp Lys Val Pro Asp
 50 55 60
 Gln Phe Leu Asp Ser Lys Ala Ser Ala Gly Ile Ser Asp Ser Ser Trp
 65 70 75 80
 Phe Pro Glu Ala Leu Ser Ser Asn Met Ser Gly Ser Phe Trp Ser Asn

85	90	95
Val Ser Ala Glu	Gly Gln Asp Leu	Ser Pro Val Ser Pro Phe Ser Glu
100	105	110
Thr Pro Gly Ser	Glu Val Phe Pro Asp Ile Ser Asp Pro Gln Val Pro	
115	120	125
Ala Lys Asp Pro Lys Pro Ser	Phe Thr Val Lys Thr Pro Ala Ser Asn	
130	135	140
Ile Ser Thr Gln Val Ser His	Thr Lys Leu Ser Val Glu Ala Pro Asp	
145	150	160
Ser Lys Phe Ser Pro Asp Asp Met Asp	Leu Lys Leu Ser Ala Gln Ser	
165	170	175
Pro Glu Ser Lys Phe Ser Ala Glu	Thr His Ser Ala Ala Ser Phe Pro	
180	185	190
Gln Gln Val Gly Gly Pro Leu Ala Val	Leu Val Gly Thr Thr Ile Arg	
195	200	205
Leu Pro Leu Val Pro Ile Pro Asn Pro Gly	Pro Pro Thr Ser Leu Val	
210	215	220
Val Trp Arg Arg Gly Ser	Lys Val Leu Ala Ala Gly Gly Leu Gly Pro	
225	230	240
Gly Ala Pro Leu Ile Ser Leu Asp Pro Ala His	Arg Asp His Leu Arg	
245	250	255
Phe Asp Gln Ala Arg Gly Val Leu Glu	Leu Ala Ser Ala Gln Leu Asp	
260	265	270
Asp Ala Gly Val Tyr Thr Ala Glu Val Ile Arg	Ala Gly Val Ser Gln	
275	280	285
Gln Thr His Glu Phe Thr Val Gly Val Tyr	Glu Pro Leu Pro Gln Leu	
290	295	300
Ser Val Gln Pro Lys Ala Pro Glu Thr Glu	Glu Gly Ala Ala Glu Leu	
305	310	320
Arg Leu Arg Cys Leu Gly Trp Gly Pro Gly	Arg Gly Glu Leu Ser Trp	
325	330	335
Ser Arg Asp Gly Arg Ala Leu Glu	Ala Ala Glu Ser Glu Gly Ala Glu	
340	345	350
Thr Pro Arg Met Arg Ser Glu Gly Asp	Gln Leu Leu Ile Val Arg Pro	
355	360	365
Val Arg Ser Asp His Ala Arg Tyr	Thr Cys Arg Val Arg Ser Pro Phe	
370	375	380
Gly His Arg Glu Ala Ala Ala Asp Val	Ser Val Phe Tyr Gly Pro Asp	
385	390	400
Pro Pro Thr Ile Thr Val Ser Ser Asp	Arg Asp Ala Ala Pro Ala Arg	
405	410	415
Phe Val Thr Ala Gly Ser Asn Val	Thr Leu Arg Cys Ala Ala Ser	
420	425	430
Arg Pro Pro Ala Asp Ile Thr Trp	Ser Leu Ala Asp Pro Ala Glu Ala	
435	440	445
Ala Val Pro Ala Gly Ser Arg	Leu Leu Leu Pro Ala Val Gly Pro Gly	
450	455	460
His Ala Gly Thr Tyr Ala Cys Leu	Ala Ala Asn Pro Arg Thr Gly Arg	
465	470	480
Arg Arg Arg Ser Leu Leu Asn Leu	Thr Val Ala Asp Leu Pro Pro Gly	
485	490	495
Ala Pro Gln Cys Ser Val Glu Gly	Gly Pro Gly Asp Arg Ser Leu Arg	
500	505	510
Phe Arg Cys Ser Trp Pro Gly Gly	Ala Pro Ala Ser Leu Gln Phe	
515	520	525
Gln Gly Leu Pro Glu Gly Ile Arg	Ala Gly Pro Val Ser Ser Val Leu	
530	535	540
Leu Ala Ala Val Pro Ala His Pro Arg	Leu Ser Gly Val Pro Ile Thr	
545	550	560

Cys Leu Ala Arg His Leu Val Ala Thr Arg Thr Cys Thr Val Thr Pro
 565 570 575
 Glu Ala Pro Arg Glu Val Leu Leu His Pro Leu Val Ala Glu Thr Arg
 580 585 590
 Leu Gly Glu Ala Glu Val Ala Leu Glu Ala Ser Gly Cys Pro Pro Pro
 595 600 605
 Ser Arg Ala Ser Trp Ala Arg Glu Gly Arg Pro Leu Ala Pro Gly Gly
 610 615 620
 Gly Ser Arg Leu Arg Leu Ser Gln Asp Gly Arg Lys Leu His Ile Gly
 625 630 635 640
 Asn Phe Ser Leu Asp Trp Asp Leu Gly Asn Tyr Ser Val Leu Cys Ser
 645 650 655
 Gly Ala Leu Gly Ala Gly Asp Gln Ile Thr Leu Ile Asp Gly Pro
 660 665 670
 Ala Leu Gly Arg Thr Ser Thr Tyr Arg Asp Trp Val Ser Leu Leu Ile
 675 680 685
 Leu Gly Pro Gln Glu Arg Ser Ala Val Val Pro Leu Pro Pro Arg Asn
 690 695 700
 Pro Gly Thr Trp Thr Phe Arg Ile Leu Pro Ile Leu Gly Gly Gln Pro
 705 710 715 720
 Gly Thr Pro Ser Gln Ser Arg Val Tyr Arg Ala Gly Pro Thr Leu Ser
 725 730 735
 His Gly Ala Ile Ala Gly Ile Val Leu Gly Ser Leu Leu Gly Leu Ala
 740 745 750
 Leu Leu Ala Val Leu Leu Leu Cys Ile Cys Cys Leu Cys Arg Phe
 755 760 765
 Arg Gly Lys Thr Pro Glu Lys Lys Lys His Pro Ser Thr Leu Val Pro
 770 775 780
 Val Val Thr Pro Ser Glu Lys Lys Met His Ser Val Thr Pro Val Glu
 785 790 795 800
 Ile Ser Trp Pro Leu Asp Leu Lys Val Pro Leu Glu Asp His Ser Ser
 805 810 815
 Thr Arg Ala Tyr Gln Ala Thr Asp Pro Ser Ser Val Val Ser Val Gly
 820 825 830
 Gly Gly Ser Lys Thr Val Arg Ala Ala Thr Gln Val
 835 840

<210> 57
 <211> 782
 <212> PRT
 <213> Homo sapiens

<400> 57

Met Asp Asn Pro Gln Ala Leu Pro Leu Phe Leu Leu Ala Ser Leu
 1 5 10 15
 Val Gly Ile Leu Thr Leu Arg Ala Ser Ser Gly Leu Gln Gln Thr Asn
 20 25 30
 Phe Ser Ser Ala Phe Ser Ser Asp Ser Lys Ser Ser Ser Gln Gly Leu
 35 40 45
 Gly Val Glu Val Pro Ser Ile Lys Pro Pro Ser Trp Lys Val Pro Asp
 50 55 60
 Gln Phe Leu Asp Ser Lys Ala Ser Ala Gly Ile Ser Asp Ser Ser Trp
 65 70 75 80
 Phe Pro Glu Ala Leu Ser Ser Asn Met Ser Gly Ser Phe Trp Ser Asn
 85 90 95
 Val Ser Ala Glu Gly Gln Asp Leu Ser Pro Val Ser Pro Phe Ser Glu
 100 105 110
 Thr Pro Gly Ser Glu Val Phe Pro Asp Ile Ser Asp Pro Gln Val Pro
 115 120 125

Ala Lys Asp Pro Lys Pro Ser Phe Thr Val Lys Thr Pro Ala Ser Asn
 130 135 140
 Ile Ser Thr Gln Val Ser His Thr Lys Leu Ser Val Glu Ala Pro Asp
 145 150 155 160
 Ser Lys Phe Ser Pro Asp Asp Met Asp Leu Lys Leu Ser Ala Gln Ser
 165 170 175
 Pro Glu Ser Lys Phe Ser Ala Glu Thr His Ser Ala Ala Ser Phe Pro
 180 185 190
 Gln Gln Val Gly Gly Pro Leu Ala Val Leu Val Gly Thr Thr Ile Arg
 195 200 205
 Leu Pro Leu Val Pro Ile Pro Asn Pro Gly Pro Pro Thr Ser Leu Val
 210 215 220
 Val Trp Arg Arg Gly Ser Lys Val Leu Ala Ala Gly Gly Leu Gly Pro
 225 230 235 240
 Gly Ala Pro Leu Ile Ser Leu Asp Pro Ala His Arg Asp His Leu Arg
 245 250 255
 Phe Asp Gln Ala Arg Gly Val Leu Glu Leu Ala Ser Ala Gln Leu Asp
 260 265 270
 Asp Ala Gly Val Tyr Thr Ala Glu Val Ile Arg Ala Gly Val Ser Gln
 275 280 285
 Gln Thr His Glu Phe Thr Val Gly Val Tyr Glu Pro Leu Pro Gln Leu
 290 295 300
 Ser Val Gln Pro Lys Ala Pro Glu Thr Glu Glu Gly Ala Ala Glu Leu
 305 310 315 320
 Arg Leu Arg Cys Leu Gly Trp Gly Pro Gly Arg Gly Glu Leu Ser Trp
 325 330 335
 Ser Arg Asp Gly Arg Ala Leu Glu Ala Ala Glu Ser Glu Gly Ala Glu
 340 345 350
 Thr Pro Arg Met Arg Ser Glu Gly Asp Gln Leu Leu Ile Val Arg Pro
 355 360 365
 Val Arg Ser Asp His Ala Arg Tyr Thr Cys Arg Val Arg Ser Pro Phe
 370 375 380
 Gly His Arg Glu Ala Ala Ala Asp Val Ser Val Phe Tyr Gly Pro Asp
 385 390 395 400
 Pro Pro Thr Ile Thr Val Ser Ser Asp Arg Asp Ala Ala Pro Ala Arg
 405 410 415
 Phe Val Thr Ala Gly Ser Asn Val Thr Leu Arg Cys Ala Ala Ser
 420 425 430
 Arg Pro Pro Ala Asp Ile Thr Trp Ser Leu Ala Asp Pro Ala Glu Ala
 435 440 445
 Ala Val Pro Ala Gly Ser Arg Leu Leu Leu Pro Ala Val Gly Pro Gly
 450 455 460
 His Ala Gly Thr Tyr Ala Cys Leu Ala Ala Asn Pro Arg Thr Gly Arg
 465 470 475 480
 Arg Arg Arg Ser Leu Leu Asn Leu Thr Val Ala Asp Leu Pro Pro Gly
 485 490 495
 Ala Pro Gln Cys Ser Val Glu Gly Pro Gly Asp Arg Ser Leu Arg
 500 505 510
 Phe Arg Cys Ser Trp Pro Gly Gly Ala Pro Ala Ala Ser Leu Gln Phe
 515 520 525
 Gln Gly Leu Pro Glu Gly Ile Arg Ala Gly Pro Val Ser Ser Val Leu
 530 535 540
 Leu Ala Ala Val Pro Ala His Pro Arg Leu Ser Gly Val Pro Ile Thr
 545 550 555 560
 Cys Leu Ala Arg His Leu Val Ala Thr Arg Thr Cys Thr Val Thr Pro
 565 570 575
 Glu Ala Pro Arg Glu Val Leu Leu His Pro Leu Val Ala Glu Thr Arg
 580 585 590
 Leu Gly Glu Ala Glu Val Ala Leu Glu Ala Ser Gly Cys Pro Pro Pro

595	600	605
Ser Arg Ala Ser Trp Ala Arg Glu Gly Arg Pro Leu Ala Pro Gly Gly		
610	615	620
Gly Ser Arg Leu Arg Leu Ser Gln Asp Gly Arg Lys Leu His Ile Gly		
625	630	635
Asn Phe Ser Leu Asp Trp Asp Leu Gly Asn Tyr Ser Val Leu Cys Ser		
645	650	655
Gly Ala Leu Gly Ala Gly Gly Asp Gln Ile Thr Leu Ile Gly Pro Thr		
660	665	670
Leu Ser His Gly Ala Ile Ala Gly Ile Val Leu Gly Ser Leu Leu Gly		
675	680	685
Leu Ala Leu Leu Ala Val Leu Leu Leu Cys Ile Cys Cys Leu Cys		
690	695	700
Arg Phe Arg Gly Lys Thr Pro Glu Lys Lys His Pro Ser Thr Leu		
705	710	715
Val Pro Val Val Thr Pro Ser Glu Lys Lys Met His Ser Val Thr Pro		
725	730	735
Val Glu Ile Ser Trp Pro Leu Asp Leu Lys Val Pro Leu Glu Asp His		
740	745	750
Ser Ser Thr Arg Ala Tyr Gln Ala Thr Asp Pro Ser Ser Val Val Ser		
755	760	765
Val Gly Gly Gly Ser Lys Thr Val Arg Ala Ala Thr Gln Val		
770	775	780

<210> 58
 <211> 262
 <212> PRT
 <213> Homo sapiens

<400> 58		
Met Asp Ser Leu Val Thr Ala Asn Thr Lys Phe Cys Phe Asp Leu Phe		
1	5	10
Gln Glu Ile Gly Lys Asp Asp Arg His Lys Asn Ile Phe Phe Ser Pro		
20	25	30
Leu Ser Leu Ser Ala Ala Leu Gly Met Val Arg Leu Gly Ala Arg Ser		
35	40	45
Asp Ser Ala His Gln Ile Asp Glu Ala Gly Ser Leu Asn Asn Glu Ser		
50	55	60
Gly Leu Val Ser Cys Tyr Phe Gly Gln Leu Leu Ser Lys Leu Asp Arg		
65	70	75
Ile Lys Thr Asp Tyr Thr Leu Ser Ile Ala Asn Arg Leu Tyr Gly Glu		
85	90	95
Gln Glu Phe Pro Ile Cys Gln Glu Tyr Leu Asp Gly Val Ile Gln Phe		
100	105	110
Tyr His Thr Thr Ile Glu Ser Val Asp Phe Gln Lys Asn Pro Glu Lys		
115	120	125
Ser Arg Gln Glu Ile Asn Phe Trp Val Glu Cys Gln Ser Gln Gly Lys		
130	135	140
Ile Lys Glu Leu Phe Ser Lys Asp Ala Ile Asn Ala Glu Thr Val Leu		
145	150	155
Val Leu Val Asn Ala Val Tyr Phe Lys Ala Lys Trp Glu Thr Tyr Phe		
165	170	175
Asp His Glu Asn Thr Val Asp Ala Pro Phe Cys Leu Asn Ala Asn Glu		
180	185	190
Asn Lys Ser Val Lys Met Met Thr Gln Lys Gly Leu Tyr Arg Ile Gly		
195	200	205
Phe Ile Glu Glu Val Lys Ala Gln Ile Leu Glu Met Arg Tyr Thr Lys		
210	215	220
Gly Lys Leu Ser Met Phe Val Leu Leu Pro Ser His Ser Lys Asp Asn		

225	230	235	240
Leu Lys Gly Leu Glu Glu Val Asn Leu His Phe His Ile Ser Thr Lys			
245	250		255
Tyr Leu Met Ile Asp Leu			
260			

<210> 59
 <211> 394
 <212> PRT
 <213> Homo sapiens

<400> 59

Met Asp Ser Leu Val Thr Ala Asn Thr Lys Phe Cys Phe Asp Leu Phe			
1	5	10	15
Gln Glu Ile Gly Lys Asp Asp Arg His Lys Asn Ile Phe Phe Ser Pro			
20	25	30	
Léu Ser Leu Ser Ala Ala Leu Gly Met Val Arg Leu Gly Ala Arg Ser			
35	40	45	
Asp Ser Ala His Gln Ile Asp Glu Val Leu His Phe Asn Lys Thr Thr			
50	55	60	
Glu Pro Leu Asp Gln Gln Ala Gly Ser Leu Asn Asn Glu Ser Gly Leu			
65	70	75	80
Val Ser Cys Tyr Phe Gly Gln Leu Leu Ser Lys Leu Asp Arg Ile Lys			
85	90	95	
Thr Asp Tyr Thr Leu Ser Ile Ala Asn Arg Leu Tyr Gly Glu Gln Glu			
100	105	110	
Phe Pro Ile Cys Gln Glu Tyr Leu Asp Gly Val Ile Gln Phe Tyr His			
115	120	125	
Thr Thr Ile Glu Ser Val Asp Phe Gln Lys Asn Pro Glu Lys Ser Arg			
130	135	140	
Gln Glu Ile Asn Phe Trp Val Glu Cys Gln Ser Gln Gly Lys Ile Lys			
145	150	155	160
Glu Leu Phe Ser Lys Asp Ala Ile Asn Ala Glu Thr Val Leu Val Leu			
165	170	175	
Val Asn Ala Val Tyr Phe Lys Ala Lys Trp Glu Thr Tyr Phe Asp His			
180	185	190	
Glu Asn Thr Val Asp Ala Pro Phe Cys Leu Asn Ala Asn Glu Asn Lys			
195	200	205	
Ser Val Lys Met Met Thr Gln Lys Gly Leu Tyr Arg Ile Gly Phe Ile			
210	215	220	
Glu Glu Val Lys Ala Gln Ile Leu Glu Met Arg Tyr Thr Lys Gly Lys			
225	230	235	240
Leu Ser Met Phe Val Leu Leu Pro Ser His Ser Lys Asp Asn Leu Lys			
245	250	255	
Gly Leu Glu Glu Leu Glu Arg Lys Ile Thr Tyr Glu Lys Met Val Ala			
260	265	270	
Trp Ser Ser Glu Asn Met Ser Glu Glu Ser Val Val Leu Ser Phe			
275	280	285	
Pro Arg Phe Thr Leu Glu Asp Ser Tyr Asp Leu Asn Ser Ile Leu Gln			
290	295	300	
Asp Met Gly Ile Thr Asp Ile Phe Asp Glu Thr Arg Ala Asp Leu Thr			
305	310	315	320
Gly Ile Ser Pro Ser Pro Asn Leu Tyr Leu Ser Lys Ile Ile His Lys			
325	330	335	
Thr Phe Val Glu Val Asp Glu Asn Gly Thr Gln Ala Ala Ala Thr			
340	345	350	
Gly Ala Val Val Ser Glu Arg Ser Leu Arg Ser Trp Val Glu Phe Asn			
355	360	365	
Ala Asn His Pro Phe Leu Phe Phe Ile Arg His Asn Lys Thr Gln Thr			

370 375 380
 Ile Leu Phe Tyr Gly Arg Val Cys Ser Pro
 385 390
 <210> 60
 <211> 471
 <212> PRT
 <213> Homo sapiens
 <400> 60
 Met Ser Val Pro Leu Leu Lys Ile Gly Val Val Leu Ser Thr Met Ala
 1 5 10 15
 Met Ile Thr Asn Trp Met Ser Gln Thr Leu Pro Ser Leu Val Gly Leu
 20 25 30
 Asn Thr Thr Lys Leu Ser Ala Ala Gly Gly Gly Thr Leu Asp Arg Ser
 35 40 45
 Thr Gly Val Leu Pro Thr Asn Pro Glu Glu Ser Trp Gln Val Tyr Ser
 50 55 60
 Ser Ala Gln Asp Ser Glu Gly Arg Cys Ile Cys Thr Val Val Ala Pro
 65 70 75 80
 Gln Gln Thr Met Cys Ser Arg Asp Ala Arg Thr Lys Gln Leu Arg Gln
 85 90 95
 Leu Leu Glu Lys Val Gln Asn Met Ser Gln Ser Ile Glu Val Leu Asp
 100 105 110
 Arg Arg Thr Gln Arg Asp Leu Gln Tyr Val Glu Lys Met Glu Asn Gln
 115 120 125
 Met Lys Gly Leu Glu Ser Lys Phe Lys Gln Ala Ile Lys Ala Lys Met
 130 135 140
 Asp Glu Leu Arg Pro Leu Ile Pro Val Leu Glu Glu Tyr Lys Ala Asp
 145 150 155 160
 Ala Lys Leu Val Leu Gln Phe Lys Glu Glu Val Gln Asn Leu Thr Ser
 165 170 175
 Val Leu Asn Glu Leu Gln Glu Glu Ile Gly Ala Tyr Asp Tyr Asp Glu
 180 185 190
 Leu Gln Ser Arg Val Ser Asn Leu Glu Arg Leu Arg Ala Cys Met
 195 200 205
 Gln Lys Leu Ala Cys Gly Lys Leu Thr Gly Ile Ser Asp Pro Val Thr
 210 215 220
 Val Lys Thr Ser Gly Ser Arg Phe Gly Ser Trp Met Thr Asp Pro Leu
 225 230 235 240
 Ala Pro Glu Gly Asp Asn Arg Val Trp Tyr Met Asp Gly Tyr His Asn
 245 250 255
 Asn Arg Phe Val Arg Glu Tyr Lys Ser Met Val Asp Phe Met Asn Thr
 260 265 270
 Asp Asn Phe Thr Ser His Arg Leu Pro His Pro Trp Ser Gly Thr Gly
 275 280 285
 Gln Val Val Tyr Asn Gly Ser Ile Tyr Phe Asn Lys Phe Gln Ser His
 290 295 300
 Ile Ile Ile Arg Phe Asp Leu Lys Thr Glu Thr Ile Leu Lys Thr Arg
 305 310 315 320
 Ser Leu Asp Tyr Ala Gly Tyr Asn Asn Met Tyr His Tyr Ala Trp Gly
 325 330 335
 Gly His Ser Asp Ile Asp Leu Met Val Asp Glu Ser Gly Leu Trp Ala
 340 345 350
 Val Tyr Ala Thr Asn Gln Asn Ala Gly Asn Ile Val Val Ser Arg Leu
 355 360 365
 Asp Pro Val Ser Leu Gln Thr Leu Gln Thr Trp Asn Thr Ser Tyr Pro
 370 375 380
 Lys Arg Ser Ala Gly Glu Ala Phe Ile Ile Cys Gly Thr Leu Tyr Val

385	390	395	400
Thr Asn Gly Tyr Ser Gly Gly Thr Lys Val His Tyr Ala Tyr Gln Thr			
405	410	415	
Asn Ala Ser Thr Tyr Glu Tyr Ile Asp Ile Pro Phe Gln Asn Lys Tyr			
420	425	430	
Ser His Ile Ser Met Leu Asp Tyr Asn Pro Lys Asp Arg Ala Leu Tyr			
435	440	445	
Ala Trp Asn Asn Gly His Gln Ile Leu Tyr Asn Val Thr Leu Phe His			
450	455	460	
Val Ile Arg Ser Asp Glu Leu			
465	470		

<210> 61
 <211> 485
 <212> PRT
 <213> Homo sapiens

<400> 61			
Met Ser Val Pro Leu Leu Lys Ile Gly Val Val Leu Ser Thr Met Ala			
1	5	10	15
Met Ile Thr Asn Trp Met Ser Gln Thr Leu Pro Ser Leu Val Gly Leu			
20	25	30	
Asn Thr Thr Lys Leu Ser Ala Ala Gly Gly Gly Thr Leu Asp Arg Ser			
35	40	45	
Thr Gly Val Leu Pro Thr Asn Pro Glu Glu Ser Trp Gln Val Tyr Ser			
50	55	60	
Ser Ala Gln Asp Ser Glu Gly Arg Cys Ile Cys Thr Val Val Ala Pro			
65	70	75	80
Gln Gln Thr Met Cys Ser Arg Asp Ala Arg Thr Lys Gln Leu Arg Gln			
85	90	95	
Leu Leu Glu Lys Val Gln Asn Met Ser Gln Ser Ile Glu Val Leu Asp			
100	105	110	
Arg Arg Thr Gln Arg Asp Leu Gln Tyr Val Glu Lys Met Glu Asn Gln			
115	120	125	
Met Lys Gly Leu Glu Ser Lys Phe Lys Gln Val Glu Glu Ile Ile Ser			
130	135	140	
Tyr Thr Trp Pro Arg Gln Phe Lys Ala Ile Lys Ala Lys Met Asp Glu			
145	150	155	160
Leu Arg Pro Leu Ile Pro Val Leu Glu Glu Tyr Lys Ala Asp Ala Lys			
165	170	175	
Leu Val Leu Gln Phe Lys Glu Glu Val Gln Asn Leu Thr Ser Val Leu			
180	185	190	
Asn Glu Leu Gln Glu Glu Ile Gly Ala Tyr Asp Tyr Asp Glu Leu Gln			
195	200	205	
Ser Arg Val Ser Asn Leu Glu Glu Arg Leu Arg Ala Cys Met Gln Lys			
210	215	220	
Leu Ala Cys Gly Lys Leu Thr Gly Ile Ser Asp Pro Val Thr Val Lys			
225	230	235	240
Thr Ser Gly Ser Arg Phe Gly Ser Trp Met Thr Asp Pro Leu Ala Pro			
245	250	255	
Glu Gly Asp Asn Arg Val Trp Tyr Met Asp Gly Tyr His Asn Asn Arg			
260	265	270	
Phe Val Arg Glu Tyr Lys Ser Met Val Asp Phe Met Asn Thr Asp Asn			
275	280	285	
Phe Thr Ser His Arg Leu Pro His Pro Trp Ser Gly Thr Gly Gln Val			
290	295	300	
Val Tyr Asn Gly Ser Ile Tyr Phe Asn Lys Phe Gln Ser His Ile Ile			
305	310	315	320
Ile Arg Phe Asp Leu Lys Thr Glu Thr Ile Leu Lys Thr Arg Ser Leu			

	325	330	335
Asp Tyr Ala Gly Tyr Asn Asn Met Tyr His Tyr Ala Trp Gly Gly His			
340	345	350	
Ser Asp Ile Asp Leu Met Val Asp Glu Ser Gly Leu Trp Ala Val Tyr			
355	360	365	
Ala Thr Asn Gln Asn			
370	375	380	
Gly Asn Ile Val Val Ser Arg Leu Asp Pro			
Val Ser Leu Gln Thr Leu Gln Thr Trp Asn Thr Ser Tyr Pro Lys Arg			
385	390	395	400
Ser Ala Gly Glu Ala Phe Ile Ile Cys Gly Thr Leu Tyr Val Thr Asn			
405	410	415	
Gly Tyr Ser Gly Gly Thr Lys Val His Tyr Ala Tyr Gln Thr Asn Ala			
420	425	430	
Ser Thr Tyr Glu Tyr Ile Asp Ile Pro Phe Gln Asn Lys Tyr Ser His			
435	440	445	
Ile Ser Met Leu Asp Tyr Asn Pro Lys Asp Arg Ala Leu Tyr Ala Trp			
450	455	460	
Asn Asn Gly His Gln Ile Leu Tyr Asn Val Thr Leu Phe His Val Ile			
465	470	475	480
Arg Ser Asp Glu Leu			
	485		

<210> 62
 <211> 286
 <212> PRT
 <213> Homo sapiens

	<400> 62		
Met Leu His Leu Leu Ala Leu Phe Leu His Cys Leu Pro Leu Ala Ser			
1	5	10	15
Gly Asp Tyr Asp Ile Cys Lys Ser Trp Val Thr Thr Asp Glu Gly Pro			
20	25	30	
Thr Trp Glu Phe Tyr Ala Cys Gln Pro Lys Val Met Arg Leu Lys Asp			
35	40	45	
Tyr Val Lys Val Lys Val Glu Pro Ser Gly Ile Thr Cys Gly Asp Pro			
50	55	60	
Pro Glu Arg Phe Cys Ser His Glu Asn Pro Tyr Leu Cys Ser Asn Glu			
65	70	75	80
Cys Asp Ala Ser Asn Pro Asp Leu Ala His Pro Pro Arg Leu Met Phe			
85	90	95	
Asp Lys Glu Glu Glu Gly Leu Ala Thr Tyr Trp Gln Ser Ile Thr Trp			
100	105	110	
Ser Arg Tyr Pro Ser Pro Leu Glu Ala Asn Ile Thr Leu Ser Trp Asn			
115	120	125	
Lys Thr Val Glu Leu Thr Asp Asp Val Val Met Thr Phe Glu Tyr Gly			
130	135	140	
Arg Pro Thr Val Met Val Leu Glu Lys Ser Leu Asp Asn Gly Arg Thr			
145	150	155	160
Trp Gln Pro Tyr Gln Phe Tyr Ala Glu Asp Cys Met Glu Ala Phe Gly			
165	170	175	
Met Ser Ala Arg Arg Ala Arg Asp Met Ser Ser Ser Ala His Arg			
180	185	190	
Val Leu Cys Thr Glu Glu Tyr Ser Arg Trp Ala Gly Ser Lys Lys Glu			
195	200	205	
Lys His Val Arg Phe Glu Val Arg Asp Arg Phe Ala Ile Phe Ala Gly			
210	215	220	
Pro Asp Leu Arg Asn Met Asp Asn Leu Tyr Thr Arg Leu Glu Ser Ala			
225	230	235	240
Lys Gly Leu Lys Glu Phe Phe Thr Leu Thr Asp Leu Arg Met Arg Leu			

245	250	255
Leu Arg Pro Ala Leu Gly Gly Thr Tyr Val Gln Arg Glu Asn Leu Tyr		
260	265	270
Lys Tyr Phe Tyr Ala Ile Ser Asn Ile Glu Val Ile Gly Arg		
275	280	285

<210> 63
 <211> 533
 <212> PRT
 <213> Homo sapiens

<400> 63
 Met Leu His Leu Leu Ala Leu Phe Leu His Cys Leu Pro Leu Ala Ser
 1 5 10 15
 Gly Asp Tyr Asp Ile Cys Lys Ser Trp Val Thr Thr Asp Glu Gly Pro
 20 25 30
 Thr Trp Glu Phe Tyr Ala Cys Gln Pro Lys Val Met Arg Leu Lys Asp
 35 40 45
 Tyr Val Lys Val Lys Val Glu Pro Ser Gly Ile Thr Cys Gly Asp Pro
 50 55 60
 Pro Glu Arg Phe Cys Ser His Glu Asn Pro Tyr Leu Cys Ser Asn Glu
 65 70 75 80
 Cys Asp Ala Ser Asn Pro Asp Leu Ala His Pro Pro Arg Leu Met Phe
 85 90 95
 Asp Lys Glu Glu Glu Gly Leu Ala Thr Tyr Trp Gln Ser Ile Thr Trp
 100 105 110
 Ser Arg Tyr Pro Ser Pro Leu Glu Ala Asn Ile Thr Leu Ser Trp Asn
 115 120 125
 Lys Thr Val Glu Leu Thr Asp Asp Val Val Met Thr Phe Glu Tyr Gly
 130 135 140
 Arg Pro Thr Val Met Val Leu Glu Lys Ser Leu Asp Asn Gly Arg Thr
 145 150 155 160
 Trp Gln Pro Tyr Gln Phe Tyr Ala Glu Asp Cys Met Glu Ala Phe Gly
 165 170 175
 Met Ser Ala Arg Arg Ala Arg Asp Met Ser Ser Ser Ser Ala His Arg
 180 185 190
 Val Leu Cys Thr Glu Glu Tyr Ser Arg Trp Ala Gly Ser Lys Lys Glu
 195 200 205
 Lys His Val Arg Phe Glu Val Arg Asp Arg Phe Ala Ile Phe Ala Gly
 210 215 220
 Pro Asp Leu Arg Asn Met Asp Asn Leu Tyr Thr Arg Leu Glu Ser Ala
 225 230 235 240
 Lys Gly Leu Lys Glu Phe Phe Thr Leu Thr Asp Leu Arg Met Arg Leu
 245 250 255
 Leu Arg Pro Ala Leu Gly Gly Thr Tyr Val Gln Arg Glu Asn Leu Tyr
 260 265 270
 Lys Tyr Phe Tyr Ala Ile Ser Asn Ile Glu Val Ile Gly Arg Cys Lys
 275 280 285
 Cys Asn Leu His Ala Asn Leu Cys Ser Met Arg Glu Gly Ser Leu Gln
 290 295 300
 Cys Glu Cys Glu His Asn Thr Thr Gly Pro Asp Cys Gly Lys Cys Lys
 305 310 315 320
 Lys Asn Phe Arg Thr Arg Ser Trp Arg Ala Gly Ser Tyr Leu Pro Leu
 325 330 335
 Pro His Gly Ser Pro Asn Ala Cys Thr Pro Pro Ser Pro Arg Glu Leu
 340 345 350
 Gly Ala Asp Cys Glu Cys Tyr Gly His Ser Asn Arg Cys Ser Tyr Ile
 355 360 365
 Asp Phe Leu Asn Val Val Thr Cys Val Ser Cys Lys His Asn Thr Arg

370	375	380
Gly Gln His Cys Gln His Cys Arg Leu Gly Tyr Tyr Arg Asn Gly Ser		
385	390	395
Ala Glu Leu Asp Asp Glu Asn Val Cys Ile Glu Cys Asn Cys Asn Gln		400
405	410	415
Ile Gly Ser Val His Asp Arg Cys Asn Glu Thr Gly Phe Cys Glu Cys		
420	425	430
Arg Glu Gly Ala Ala Gly Pro Lys Cys Asp Asp Cys Leu Pro Thr His		
435	440	445
Tyr Trp Arg Gln Gly Cys Tyr Pro Asn Val Cys Asp Asp Asp Gln Leu		
450	455	460
Leu Cys Gln Asn Gly Gly Thr Cys Leu Gln Asn Gln Arg Cys Ala Cys		
465	470	475
Pro Arg Gly Tyr Thr Gly Val Arg Cys Glu Gin Pro Arg Cys Asp Pro		480
485	490	495
Ala Asp Asp Asp Gly Gly Leu Asp Cys Asp Arg Ala Pro Gly Ala Ala		
500	505	510
Pro Arg Pro Ala Thr Leu Leu Gly Cys Leu Leu Leu Leu Gly Leu Ala		
515	520	525
Ala Arg Leu Gly Arg		
530		

<210> 64
 <211> 495
 <212> PRT
 <213> Homo sapiens

<400> 64			
Met Phe Ala Asn Ser Pro Gly Cys Ser Asn Met Leu His Tyr Val Tyr			
1	5	10	15
Cys Ala Cys Gly His Gly Leu Gln Leu Val Arg Ser Val Ser Ser Ser			
20	25		30
Val Asp Glu Gly Gly Thr Cys His Cys Met Val His Leu Pro Asn Asn			
35	40		45
Pro Ile Pro Leu Glu Gln Leu Glu Gln Leu Gln Ser Thr Ala Gln Glu			
50	55		60
Leu Ile Cys Lys Tyr Glu Gln Lys Leu Ser Arg Cys Ala Arg Ala Ile			
65	70	75	80
Glu Asp Lys Asp Asn Glu Val Leu Glu Met Ser His Met Leu Lys Ser			
85	90		95
Trp Asn Pro Ser Ala Leu Ala Ser Pro Tyr Glu Asn Pro Gly Phe Asn			
100	105		110
Leu Leu Cys Leu Glu Leu Glu Gly Ala Gln Glu Leu Val Thr Gln Leu			
115	120		125
Lys Ala Met Gly Gly Val Ser Val Ala Gly Asp Leu Leu His Gln Leu			
130	135		140
Gln Ser Gln Val Thr Asn Ala Ser Leu Thr Leu Lys Leu Leu Ala Asp			
145	150	155	160
Ser Asp Gln Cys Ser Phe Gly Ala Leu Gln Gln Glu Val Asp Val Leu			
165	170		175
Glu Ser Gln Leu Ser Glu Cys Glu Arg Glu Lys Glu Lys Glu Gly Leu			
180	185		190
Trp Thr Pro Trp Thr Thr Pro Pro Pro Ala Ser Cys Ala His Gly Gly			
195	200		205
Leu Gln Glu Val Ser Lys Ser Leu Val Val Gln Leu Thr Arg Arg Gly			
210	215		220
Phe Ser Tyr Lys Ala Gly Pro Trp Gly Arg Asp Ser Ala Pro Asn Pro			
225	230	235	240
Ala Ser Ser Leu Tyr Trp Val Ala Pro Leu Arg Thr Asp Gly Arg Tyr			

245	250	255
Phe Asp Tyr Tyr Arg Leu Pro Pro Ser Tyr Asn Asp Leu Ala	Leu Met	
260	265	270
Lys Asn Tyr Glu Glu Arg Lys Met Gly Tyr Gly Asp Gly Ser Gly Asn		
275	280	285
Val Val Tyr Lys Asn Phe Met Tyr Phe Asn Tyr Cys Gly Thr Ser Asp		
290	295	300
Met Ala Lys Met Asp Leu Ser Ser Asn Thr Leu Val Leu Trp Arg Leu		
305	310	315
Leu Pro Gly Ala Thr Tyr Asn Asn Arg Phe Ser Cys Ala Gly Val Pro		
325	330	335
Trp Lys Asp Leu Asp Phe Ala Gly Asp Glu Lys Gly Leu Trp Val Leu		
340	345	350
Tyr Ala Thr Glu Glu Ser Lys Gly Asn Leu Val Val Ser Arg Leu Asn		
355	360	365
Ala Ser Thr Leu Glu Val Glu Lys Thr Trp Arg Thr Ser Gln Tyr Lys		
370	375	380
Pro Ala Leu Ser Gly Ala Phe Met Ala Cys Gly Val Leu Tyr Ala Leu		
385	390	395
His Ser Leu Asn Thr His Gln Glu Glu Ile Phe Tyr Ala Phe Asp Thr		
405	410	415
Thr Thr Gly Gln Glu Arg Arg Leu Ser Ile Leu Leu Asp Lys Met Leu		
420	425	430
Glu Lys Leu Gln Gly Ile Asn Tyr Cys Pro Ser Asp His Lys Pro Tyr		
435	440	445
Val Phe Ser Asp Gly Tyr Leu Ile Asn Tyr Asp Leu Thr Phe Leu Thr		
450	455	460
Met Lys Thr Arg Leu Pro Arg Pro Pro Thr Arg Arg Pro Ser Gly Ala		
465	470	475
His Ala Pro Pro Lys Pro Val Lys Pro Asn Glu Ala Ser Arg Pro		
485	490	495

<210> 65
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 65		
Met Arg Asn His Lys Lys Val Thr Asn Ala Ser Leu Thr Leu Lys Leu		
1	5	10
Leu Ala Asp Ser Asp Gln Cys Ser Phe Gly Ala Leu Gln Gln Glu Val		
20	25	30
Asp Val Leu Glu Ser Gln Leu Ser Glu Ser Ser Cys Ala His Gly Gly		
35	40	45
Leu Gln Glu Val Ser Lys Ser Leu Val Val Gln Leu Thr Arg Arg Gly		
50	55	60
Phe Ser Tyr Lys Ala Gly Pro Trp Gly Arg Asp Ser Ala Pro Asn Pro		
65	70	75
Ala Ser Ser Leu Tyr Trp Val Ala Pro Leu Arg Thr Asp Gly Ser Tyr		
85	90	95
Gly Cys His Pro Ile Ile Leu Asn Ala Gly Thr Trp Pro Arg Tyr Phe		
100	105	110
Asp Tyr Tyr Arg Leu Cys Lys Ser Tyr Asn Asp Leu Ala Leu Leu Lys		
115	120	125
Asn Tyr Glu Glu Arg Lys Met Gly Tyr Gly Asp Gly Ser Gly Asn Val		
130	135	140
Val Tyr Lys Asn Phe Met Tyr Phe Asn Tyr Cys Gly Thr Ser Asp Met		
145	150	155
Ala Lys Met Asp Leu Ser Ser Asn Thr Leu Val Leu Trp Arg Leu Leu		

165	170	175	
Pro Gly Ala Thr Tyr Asn Asn Arg Phe Ser Cys Ala Gly Val Pro Trp			
180	185	190	
Lys Asp Leu Asp Phe Ala Gly Asp Glu Lys Gly Leu Trp Val Leu Tyr			
195	200	205	
Ala Thr Glu Glu Ser Lys Gly Asn Leu Val Val Ser Arg Leu Asn Ala			
210	215	220	
Ser Thr Leu Glu Val Glu Lys Thr Trp Arg Thr Ser Gln Tyr Lys Pro			
225	230	235	240
Ala Leu Ser Gly Ala Phe Met Ala Cys Gly Val Leu Tyr Ala Leu His			
245	250	255	
Ser Leu Asn Thr His Gln Glu Glu Ile Phe Tyr Ala Phe Asp Thr Thr			
260	265	270	
Thr Gly Gln Glu Arg Arg Leu Ser Ile Leu Leu Asp Lys Met Leu Glu			
275	280	285	
Lys Leu Gln Gly Ile Asn Tyr Cys Pro Ser Asp His Lys Pro Tyr Val			
290	295	300	
Phe Ser Asp Gly Tyr Leu Ile Asn Tyr Asp Leu Thr Phe Leu Thr Met			
305	310	315	320
Lys Thr Arg Leu Pro Arg Pro Pro Thr Arg Arg Pro Ser Gly Ala His			
325	330	335	
Ala Pro Pro Lys Pro Val Lys Pro Asn Glu Ala Ser Arg Pro			
340	345	350	

<210> 66
 <211> 619
 <212> PRT
 <213> Homo sapiens

<400> 66			
Met Gly Arg Gly Arg Ala Leu Leu Pro Ile Glu Met Leu Gln Leu Ser			
1	5	10	15
Leu Arg Glu Glu Ser Asp Thr Ala Arg Met Gly Ala Gln Glu Gln Ile			
20	25	30	
Gly Leu Gln Asp Glu Ile Gln Ala Ala Asn Ala Gly Ile Ser Gly Ser			
35	40	45	
Pro Gly Val Asp Gly Val Val Asp Gly Gly Ser Ser Arg Gly Asp Pro			
50	55	60	
Ala Leu Thr Val Ser Val Cys Glu Val Pro Pro Val Arg Ser Pro Phe			
65	70	75	80
Arg Thr His Pro Gln Leu Pro Val Arg Leu Pro Arg Asn Leu Glu Phe			
85	90	95	
Ser Val Pro Glu Arg Arg Thr Leu Arg Asn Arg Leu Thr Ser Ala Thr			
100	105	110	
Leu Ala Pro Pro Thr Arg His Met Leu Leu Leu Leu Leu Leu Pro			
115	120	125	
Pro Leu Leu Cys Gly Arg Val Gly Ala Lys Glu Gln Lys Asp Tyr Leu			
130	135	140	
Leu Thr Met Gln Lys Ser Val Thr Val Gln Glu Gly Leu Cys Val Ser			
145	150	155	160
Val Leu Cys Ser Phe Ser Tyr Pro Gln Asn Gly Trp Thr Ala Ser Asp			
165	170	175	
Pro Val His Gly Tyr Trp Phe Arg Ala Gly Asp His Val Ser Arg Asn			
180	185	190	
Ile Pro Val Ala Thr Asn Asn Pro Ala Arg Ala Val Gln Glu Glu Thr			
195	200	205	
Arg Asp Arg Phe His Leu Leu Gly Asp Pro Gln Asn Lys Asp Cys Thr			
210	215	220	
Leu Ser Ile Arg Asp Thr Arg Glu Ser Asp Ala Gly Thr Tyr Val Phe			

225 230 235 240
 Cys Val Glu Arg Gly Asn Met Lys Trp Asn Tyr Lys Tyr Asp Gln Leu
 245 250 255
 Ser Val Asn Val Thr Ala Leu Thr His Met Pro Thr Phe Ser Ile Pro
 260 265 270
 Gly Thr Leu Glu Ser Gly His Pro Arg Asn Leu Thr Cys Ser Val Pro
 275 280 285
 Trp Ala Cys Glu Gln Gly Thr Pro Pro Thr Ile Thr Trp Met Gly Ala
 290 295 300
 Ser Val Ser Ser Leu Asp Pro Thr Ile Thr Arg Ser Ser Met Leu Ser
 305 310 315 320
 Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser Leu Thr Cys Gln Val
 325 330 335
 Thr Leu Pro Gly Ala Gly Val Thr Met Thr Arg Ala Val Arg Leu Asn
 340 345 350
 Ile Ser Tyr Pro Pro Gln Asn Leu Thr Met Thr Val Phe Gln Gly Asp
 355 360 365
 Gly Thr Ala Ser Thr Thr Leu Arg Asn Gly Ser Ala Leu Ser Val Leu
 370 375 380
 Glu Gly Gln Ser Leu His Leu Val Cys Ala Val Asp Ser Asn Pro Pro
 385 390 395 400
 Ala Arg Leu Ser Trp Thr Trp Gly Ser Leu Thr Leu Ser Pro Ser Gln
 405 410 415
 Ser Ser Asn Leu Gly Val Leu Glu Leu Pro Arg Val His Val Lys Asp
 420 425 430
 Glu Gly Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln His
 435 440 445
 Ile Ser Leu Ser Leu Ser Leu Gln Asn Glu Tyr Thr Gly Lys Met Arg
 450 455 460
 Pro Ile Ser Gly Val Thr Leu Gly Ala Phe Gly Gly Ala Gly Ala Thr
 465 470 475 480
 Ala Leu Val Phe Leu Tyr Phe Cys Ile Ile Phe Val Val Val Arg Ser
 485 490 495
 Cys Arg Lys Lys Ser Ala Arg Pro Ala Val Gly Val Gly Asp Thr Gly
 500 505 510
 Met Glu Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Met Glu Glu
 515 520 525
 Gly Thr Pro Gly Pro Pro Ser Trp Met Leu Ser Gly Ala Cys Trp Pro
 530 535 540
 His Cys Ser Ala Leu Thr Pro Phe Ser Ser Ser Ile Gln Gly Pro Leu
 545 550 555 560
 Ile Glu Ser Pro Ala Asp Asp Ser Pro Pro His His Ala Pro Pro Ala
 565 570 575
 Leu Ala Thr Pro Ser Pro Glu Glu Gly Glu Ile Gln Tyr Ala Ser Leu
 580 585 590
 Ser Phe His Lys Ala Arg Pro Gln Tyr Pro Gln Glu Gln Glu Ala Ile
 595 600 605
 Gly Tyr Glu Tyr Ser Glu Ile Asn Ile Pro Lys
 610 615

<210> 67
 <211> 490
 <212> PRT
 <213> Homo sapiens

<400> 67

Met Leu Leu Leu Leu Leu Leu Pro Pro Leu Leu Cys Gly Arg Val
 1 5 10 15
 Gly Ala Lys Glu Gln Lys Asp Tyr Leu Leu Thr Met Gln Lys Ser Val

20	25	30
Thr Val Gln Glu Gly Leu Cys Val Ser Val Leu Cys Ser Phe Ser Tyr		
35	40	45
Pro Gln Asn Gly Trp Thr Ala Ser Asp Pro Val His Gly Tyr Trp Phe		
50	55	60
Arg Ala Gly Asp His Val Ser Arg Asn Ile Pro Val Ala Thr Asn Asn		
65	70	75
Pro Ala Arg Ala Val Gln Glu Glu Thr Arg Asp Arg Phe His Leu Leu		
85	90	95
Gly Asp Pro Gln Asn Lys Asp Cys Thr Leu Ser Ile Arg Asp Thr Arg		
100	105	110
Glu Ser Asp Ala Gly Thr Tyr Val Phe Cys Val Glu Arg Gly Asn Met		
115	120	125
Lys Trp Asn Tyr Lys Tyr Asp Gln Leu Ser Val Asn Val Thr Ala Leu		
130	135	140
Thr His Met Pro Thr Phe Ser Ile Pro Gly Thr Leu Glu Ser Gly His		
145	150	155
Pro Arg Asn Leu Thr Cys Ser Val Pro Trp Ala Cys Glu Gln Gly Thr		
165	170	175
Pro Pro Thr Ile Thr Trp Met Gly Ala Ser Val Ser Ser Leu Asp Pro		
180	185	190
Thr Ile Thr Arg Ser Ser Met Leu Ser Leu Ile Pro Gln Pro Gln Asp		
195	200	205
His Gly Thr Ser Leu Thr Cys Gln Val Thr Leu Pro Gly Ala Gly Val		
210	215	220
Thr Met Thr Arg Ala Val Arg Leu Asn Ile Ser Tyr Pro Pro Gln Asn		
225	230	235
Leu Thr Met Thr Val Phe Gln Gly Asp Gly Thr Ala Ser Thr Thr Leu		
245	250	255
Arg Asn Gly Ser Ala Leu Ser Val Leu Glu Gly Gln Ser Leu His Leu		
260	265	270
Val Cys Ala Val Asp Ser Asn Pro Pro Ala Arg Leu Ser Trp Thr Trp		
275	280	285
Gly Ser Leu Thr Leu Ser Pro Ser Gln Ser Ser Asn Leu Gly Val Leu		
290	295	300
Glu Leu Pro Arg Val His Val Lys Asp Glu Gly Glu Phe Thr Cys Arg		
305	310	315
Ala Gln Asn Pro Leu Gly Ser Gln His Ile Ser Leu Ser Leu Ser Leu		
325	330	335
Gln Asn Glu Tyr Thr Gly Lys Met Arg Pro Ile Ser Gly Val Thr Leu		
340	345	350
Gly Ala Phe Gly Gly Ala Gly Ala Thr Ala Leu Val Phe Leu Tyr Phe		
355	360	365
Cys Ile Ile Phe Val Val Val Arg Ser Cys Arg Lys Lys Ser Ala Arg		
370	375	380
Pro Ala Val Gly Val Gly Asp Thr Gly Met Glu Asp Ala Asn Ala Val		
385	390	395
Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr Glu Ser Trp Lys Asp Gly		
405	410	415
Asn Pro Leu Lys Lys Pro Pro Ala Val Ala Pro Ser Ser Gly Glu		
420	425	430
Glu Gly Glu Leu His Tyr Ala Thr Leu Ser Phe His Lys Val Lys Pro		
435	440	445
Gln Asp Pro Gln Gly Gln Glu Ala Thr Asp Ser Glu Tyr Ser Glu Ile		
450	455	460
Lys Ile His Lys Arg Glu Thr Ala Glu Thr Gln Ala Cys Leu Arg Asn		
465	470	475
His Asn Pro Ser Ser Lys Glu Val Arg Gly		
485	490	495

<210> 68
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly
 1 5 10 15
 Lys Glu Val Cys Tyr Glu Arg Leu Gly Cys Phe Ser Asp Asp Ser Pro
 20 25 30
 Trp Ser Gly Ile Thr Glu Arg Pro Leu His Ile Leu Pro Trp Ser Pro
 35 40 45
 Lys Asp Val Asn Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn
 50 55 60
 Asn Phe Gln Glu Ile Ser Ala Val Asn Ser Ser Thr Ile Gln Ala Ser
 65 70 75 80
 Tyr Phe Gly Thr Asp Lys Ile Thr Arg Ile Asn Ile Ala Gly Trp Lys
 85 90 95
 Thr Asp Gly Lys Trp Gln Arg Asp Met Cys Asn Val Leu Leu Gln Leu
 100 105 110
 Glu Asp Ile Asn Cys Ile Asn Leu Asp Trp Ile Asn Gly Ser Arg Glu
 115 120 125
 Tyr Ile His Ala Val Asn Asn Leu Arg Val Val Gly Ala Glu Val Ala
 130 135 140
 Tyr Phe Ile Asp Val Leu Met Lys Lys Phe Glu Tyr Ser Pro Ser Lys
 145 150 155 160
 Val His Leu Ile Gly His Ser Leu Gly Ala His Leu Ala Gly Glu Ala
 165 170 175
 Gly Ser Arg Ile Pro Gly Leu Gly Arg Ile Thr Gly Lys His Ala Leu
 180 185 190
 Gln Leu Gly Leu Glu Cys Ala Thr Glu Gly Tyr Leu Leu Ser Ala Thr
 195 200 205
 Leu Ala Asn Asn Val Asn Phe Val Asp Thr Asn His Met Asp Ala Thr
 210 215 220
 Pro Ile Ile Pro Gln Trp Met Arg Gly Thr Ser Gly Thr Ser Asn Pro
 225 230 235 240
 Leu Pro Val Thr Ser Ser Leu Cys Leu Trp Leu Ala Asp Leu Gly Ser
 245 250 255
 Val Ser Leu Val Cys Leu Trp Pro Glu Met Ala Ser Phe Phe Asp Cys
 260 265 270
 Asn His Ala Arg Ser Tyr Gln Phe Tyr Ala Glu Ser Ile Leu Asn Pro
 275 280 285
 Asp Ala Phe Ile Ala Tyr Pro Cys Arg Ser Tyr Thr Ser Phe Lys Ala
 290 295 300
 Gly Asn Cys Phe Phe Cys Ser Lys Glu Gly Cys Pro Thr Met Gly His
 305 310 315 320
 Phe Ala Asp Arg Phe His Phe Lys Asn Met Lys Thr Asn Gly Ser His
 325 330 335
 Tyr Phe Leu Asn Thr Gly Ser Leu Ser Pro Phe Ala Arg Trp Arg His
 340 345 350
 Lys Leu Ser Val Lys Leu Ser Gly Ser Glu Val Thr Gln Gly Thr Val
 355 360 365
 Phe Leu Arg Val Gly Gly Ala Val Arg Lys Thr Gly Glu Phe Ala Ile
 370 375 380
 Val Ser Gly Lys Leu Glu Pro Gly Met Thr Tyr Thr Lys Leu Ile Asp
 385 390 395 400
 Ala Asp Val Asn Val Gly Asn Ile Thr Ser Val Gln Phe Ile Trp Lys
 405 410 415

Lys His Leu Phe Glu Asp Ser Gln Asn Lys Leu Gly Ala Glu Met Val
 420 425 430
 Ile Asn Thr Ser Gly Lys Tyr Gly Tyr Lys Ser Thr Phe Cys Ser Gln
 435 440 445
 Asp Ile Met Gly Pro Asn Ile Leu Gln Asn Leu Lys Pro Cys
 450 455 460

<210> 69
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 69
 Met Val Leu Leu Leu Val Ile Leu Ile Pro Val Leu Val Ser Ser Ala
 1 5 10 15
 Gly Thr Ser Ala His Tyr Glu Met Leu Gly Thr Cys Arg Met Val Cys
 20 25 30
 Asp Pro Tyr Gly Gly Thr Lys Ala Pro Ser Thr Ala Ala Thr Pro Asp
 35 40 45
 Arg Gly Leu Met Gln Ser Leu Pro Thr Phe Ile Gln Gly Pro Lys Gly
 50 55 60
 Glu Ala Gly Arg Pro Gly Lys Ala Gly Pro Arg Gly Pro Pro Gly Glu
 65 70 75 80
 Pro Gly Pro Pro Gly Pro Met Gly Pro Pro Gly Glu Lys Gly Glu Pro
 85 90 95
 Gly Arg Gln Gly Leu Pro Gly Pro Pro Gly Ala Pro Gly Leu Asn Ala
 100 105 110
 Ala Gly Ala Ile Ser Ala Ala Thr Tyr Ser Thr Gly Pro Lys Ile Ala
 115 120 125
 Phe Tyr Ala Gly Leu Lys Arg Gln His Glu Gly Tyr Glu Val Leu Lys
 130 135 140
 Phe Asp Asp Val Val Thr Asn Leu Gly Asn His Tyr Asp Pro Thr Thr
 145 150 155 160
 Gly Lys Phe Thr Cys Ser Ile Pro Gly Ile Tyr Phe Phe Thr Tyr His
 165 170 175
 Val Leu Met Arg Gly Gly Asp Gly Thr Ser Met Trp Ala Asp Leu Cys
 180 185 190
 Lys Asn Asn Gln Val Arg Ala Ser Ala Ile Ala Gln Asp Ala Asp Gln
 195 200 205
 Asn Tyr Asp Tyr Ala Ser Asn Ser Val Val Leu His Leu Glu Pro Gly
 210 215 220
 Asp Glu Val Tyr Ile Lys Leu Asp Gly Gly Lys Ala His Gly Gly Asn
 225 230 235 240
 Asn Asn Lys Tyr Ser Thr Phe Ser Gly Phe Ile Ile Tyr Ala Asp
 245 250 255

<210> 70
 <211> 784
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Glu Gly Asp Gly Gly Thr Pro Trp Ala Leu Ala Leu Leu Arg Thr
 1 5 10 15
 Phe Asp Ala Gly Glu Phe Thr Gly Trp Glu Lys Val Gly Ser Gly Gly
 20 25 30
 Phe Gly Gln Val Tyr Lys Val Arg His Val His Trp Lys Thr Trp Leu
 35 40 45
 Ala Ile Lys Cys Ser Pro Ser Leu His Val Asp Asp Arg Glu Arg Met

50	55	60													
Glu	Leu	Leu	Glu	Glu	Ala	Lys	Lys	Met	Glu	Met	Ala	Lys	Phe	Arg	Tyr
65					70		75			75					80
Ile	Leu	Pro	Val	Tyr	Gly	Ile	Cys	Arg	Glu	Pro	Val	Gly	Leu	Val	Met
						85			90					95	
Glu	Tyr	Met	Glu	Thr	Gly	Ser	Leu	Glu	Lys	Leu	Leu	Ala	Ser	Glu	Pro
						100			105					110	
Leu	Pro	Trp	Asp	Leu	Arg	Phe	Arg	Ile	Ile	His	Glu	Thr	Ala	Val	Gly
						115			120					125	
Met	Asn	Phe	Leu	His	Cys	Met	Ala	Pro	Pro	Leu	Leu	His	Leu	Asp	Leu
						130			135					140	
Lys	Pro	Ala	Asn	Ile	Leu	Leu	Asp	Ala	His	Tyr	His	Val	Lys	Ile	Ser
						145			150				155		160
Asp	Phe	Gly	Leu	Ala	Lys	Cys	Asn	Gly	Leu	Ser	His	Ser	His	Asp	Leu
						165			170					175	
Ser	Met	Asp	Gly	Leu	Phe	Gly	Thr	Ile	Ala	Tyr	Leu	Pro	Pro	Glu	Arg
						180			185					190	
Ile	Arg	Glu	Lys	Ser	Arg	Leu	Phe	Asp	Thr	Lys	His	Asp	Val	Tyr	Ser
						195			200					205	
Phe	Ala	Ile	Val	Ile	Trp	Gly	Val	Leu	Thr	Gln	Lys	Lys	Pro	Phe	Ala
						210			215					220	
Asp	Glu	Lys	Asn	Ile	Leu	His	Ile	Met	Val	Lys	Val	Val	Lys	Gly	His
						225			230				235		240
Arg	Pro	Glu	Leu	Pro	Pro	Val	Cys	Arg	Ala	Arg	Pro	Arg	Ala	Cys	Ser
						245			250					255	
His	Leu	Ile	Arg	Leu	Met	Gln	Arg	Cys	Trp	Gln	Gly	Asp	Pro	Arg	Val
						260			265					270	
Arg	Pro	Thr	Phe	Gln	Glu	Ile	Thr	Ser	Glu	Thr	Glu	Asp	Leu	Cys	Glu
						275			280					285	
Lys	Pro	Asp	Asp	Glu	Val	Lys	Glu	Thr	Ala	His	Asp	Leu	Asp	Val	Lys
						290			295					300	
Ser	Pro	Pro	Glu	Pro	Arg	Ser	Glu	Val	Val	Pro	Ala	Arg	Leu	Lys	Arg
						305			310				315		320
Ala	Ser	Ala	Pro	Thr	Phe	Asp	Asn	Asp	Tyr	Ser	Leu	Ser	Glu	Leu	Leu
						325			330					335	
Ser	Gln	Leu	Asp	Ser	Gly	Val	Ser	Gln	Ala	Val	Glu	Gly	Pro	Glu	Glu
						340			345					350	
Leu	Ser	Arg	Ser	Ser	Ser	Glu	Ser	Lys	Leu	Pro	Ser	Ser	Gly	Ser	Gly
						355			360				365		
Lys	Arg	Leu	Ser	Gly	Val	Ser	Ser	Val	Asp	Ser	Ala	Phe	Ser	Ser	Arg
						370			375				380		
Gly	Ser	Leu	Ser	Leu	Ser	Phe	Glu	Arg	Glu	Pro	Ser	Thr	Ser	Asp	Leu
						385			390				395		400
Gly	Thr	Thr	Asp	Val	Gln	Lys	Lys	Lys	Leu	Val	Asp	Ala	Ile	Val	Ser
						405			410					415	
Gly	Asp	Thr	Ser	Lys	Leu	Met	Lys	Ile	Leu	Gln	Pro	Gln	Asp	Val	Asp
						420			425				430		
Leu	Ala	Leu	Asp	Ser	Gly	Ala	Ser	Leu	Leu	His	Leu	Ala	Val	Glu	Ala
						435			440				445		
Gly	Gln	Glu	Glu	Cys	Ala	Lys	Trp	Leu	Leu	Leu	Asn	Asn	Ala	Asn	Pro
						450			455				460		
Asn	Leu	Ser	Asn	Arg	Arg	Gly	Ser	Thr	Pro	Leu	His	Met	Ala	Val	Glu
						465			470				475		480
Arg	Arg	Val	Arg	Gly	Val	Val	Glu	Leu	Leu	Leu	Ala	Arg	Lys	Ile	Ser
						485			490				495		
Val	Asn	Ala	Lys	Asp	Glu	Asp	Gln	Trp	Thr	Ala	Leu	His	Phe	Ala	Ala
						500			505				510		
Gln	Asn	Gly	Asp	Glu	Ser	Ser	Thr	Arg	Leu	Leu	Leu	Glu	Lys	Asn	Ala
						515			520				525		

Ser Val Asn Glu Val Asp Phe Glu Gly Arg Thr Pro Met His Val Ala
 530 535 540
 Cys Gln His Gly Gln Glu Asn Ile Val Arg Ile Leu Leu Arg Arg Gly
 545 550 555 560
 Val Asp Val Ser Leu Gln Gly Lys Asp Ala Trp Leu Pro Leu His Tyr
 565 570 575
 Ala Ala Trp Gln Gly His Leu Pro Ile Val Lys Leu Ala Lys Gln
 580 585 590
 Pro Gly Val Ser Val Asn Ala Gln Thr Leu Asp Gly Arg Thr Pro Leu
 595 600 605
 His Leu Ala Ala Gln Arg Gly His Tyr Arg Val Ala Arg Ile Leu Ile
 610 615 620
 Asp Leu Cys Ser Asp Val Asn Val Cys Ser Leu Leu Ala Gln Thr Pro
 625 630 635 640
 Leu His Val Ala Ala Glu Thr Gly His Thr Ser Thr Ala Arg Leu Leu
 645 650 655
 Leu His Arg Gly Ala Gly Lys Glu Ala Met Thr Ser Asp Gly Tyr Thr
 660 665 670
 Ala Leu His Leu Ala Ala Arg Asn Gly His Leu Ala Thr Val Lys Leu
 675 680 685
 Leu Val Glu Glu Lys Ala Asp Val Leu Ala Arg Gly Pro Leu Asn Gln
 690 695 700
 Thr Ala Leu His Leu Ala Ala Ala His Gly His Ser Glu Val Val Glu
 705 710 715 720
 Glu Leu Val Ser Ala Asp Val Ile Asp Leu Phe Asp Glu Gln Gly Leu
 725 730 735
 Ser Ala Leu His Leu Ala Ala Gln Gly Arg His Ala Gln Thr Val Glu
 740 745 750
 Thr Leu Leu Arg His Gly Ala His Ile Asn Leu Gln Ser Leu Lys Phe
 755 760 765
 Gln Gly Gly His Gly Pro Ala Ala Thr Leu Leu Arg Arg Ser Lys Thr
 770 775 780

<210> 71
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Ala Ala Pro Ala Leu Leu Leu Ala Leu Leu Leu Pro Val Gly
 1 5 10 15
 Ala Trp Pro Gly Leu Pro Arg Arg Pro Cys Val His Cys Cys Arg Pro
 20 25 30
 Ala Trp Pro Pro Gly Pro Tyr Ala Arg Val Ser Asp Arg Asp Leu Trp
 35 40 45
 Arg Gly Asp Leu Trp Arg Gly Leu Pro Arg Val Arg Pro Thr Ile Asp
 50 55 60
 Ile Glu Ile Leu Lys Gly Glu Lys Gly Glu Ala Gly Val Arg Gly Arg
 65 70 75 80
 Ala Gly Arg Ser Gly Lys Glu Gly Pro Pro Gly Ala Arg Gly Leu Gln
 85 90 95
 Gly Arg Arg Gly Gln Lys Gly Gln Val Gly Pro Pro Gly Ala Ala Cys
 100 105 110
 Arg Arg Ala Tyr Ala Ala Phe Ser Val Gly Arg Arg Glu Gly Leu His
 115 120 125
 Ser Ser Asp His Phe Gln Ala Val Pro Phe Asp Thr Glu Leu Val Asn
 130 135 140
 Leu Asp Gly Ala Phe Asp Leu Ala Ala Gly Arg Phe Leu Cys Thr Val
 145 150 155 160

Pro Gly Val Tyr Phe Leu Ser Leu Asn Val His Thr Trp Asn Tyr Lys
 165 170 175
 Glu Thr Tyr Leu His Ile Met Leu Asn Arg Arg Pro Ala Ala Val Leu
 180 185 190
 Tyr Ala Gln Pro Ser Glu Arg Ser Val Met Gln Ala Gln Ser Leu Met
 195 200 205
 Leu Leu Leu Ala Ala Gly Asp Ala Val Trp Val Arg Met Phe Gln Arg
 210 215 220
 Asp Arg Asp Asn Ala Ile Tyr Gly Glu His Gly Asp Leu Tyr Ile Thr
 225 230 235 240
 Phe Ser Gly His Leu Val Lys Pro Ala Ala Glu Leu
 245 250

<210> 72
 <211> 593
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Pro Ser Ser Leu Phe Ala Asp Leu Glu Arg Asn Gly Ser Gly Gly
 1 5 10 15
 Gly Gly Gly Gly Ser Ser Gly Gly Glu Thr Leu Asp Asp Gln Arg
 20 25 30
 Ala Leu Gln Leu Ala Leu Asp Gln Leu Ser Leu Leu Gly Leu Asp Ser
 35 40 45
 Asp Glu Gly Ala Ser Leu Tyr Asp Ser Glu Pro Arg Lys Lys Ser Val
 50 55 60
 Asn Met Thr Glu Cys Val Pro Val Pro Ser Ser Glu His Val Ala Glu
 65 70 75 80
 Ile Val Gly Arg Gln Gly Arg Ser Arg Arg Asp Gly Glu Leu Asp Pro
 85 90 95
 Ser Gly Ile Ser Pro Asp Asp Phe Ser Gly Ile Leu Gly Phe Gly Ser
 100 105 110
 Gly Arg Leu Gln Ser Leu Gly Glu Gly Gln Ala Ala Asn Gly Leu Phe
 115 120 125
 Leu Glu Arg Leu Ala Gly Gly Ile Arg Cys Pro Ala Arg Gly Ala Ala
 130 135 140
 Arg Gly Cys Lys Ile Lys Ala Leu Arg Ala Lys Thr Asn Thr Tyr Ile
 145 150 155 160
 Lys Thr Pro Val Arg Gly Glu Glu Pro Val Phe Val Val Thr Gly Arg
 165 170 175
 Lys Glu Asp Val Ala Met Ala Arg Arg Glu Ile Ile Ser Ala Ala Glu
 180 185 190
 His Phe Ser Met Ile Arg Ala Ser Arg Asn Lys Asn Thr Ala Leu Asn
 195 200 205
 Gly Ala Val Pro Gly Pro Pro Asn Leu Pro Gly Gln Thr Thr Ile Gln
 210 215 220
 Val Arg Val Pro Tyr Arg Val Val Gly Leu Val Val Gly Pro Lys Gly
 225 230 235 240
 Ala Thr Ile Lys Arg Ile Gln Gln Thr His Thr Tyr Ile Val Thr
 245 250 255
 Pro Ser Arg Asp Lys Glu Pro Val Phe Glu Val Thr Gly Met Pro Glu
 260 265 270
 Asn Val Asp Arg Ala Arg Glu Glu Ile Glu Ala His Ile Ala Leu Arg
 275 280 285
 Thr Gly Gly Ile Ile Glu Leu Thr Asp Glu Asn Asp Phe His Ala Asn
 290 295 300
 Gly Thr Asp Val Gly Phe Asp Leu His His Gly Ser Gly Gly Ala Ser
 305 310 315 320

Thr Asp Ser Tyr Phe Gly Gly Thr Ser Ser Ser Ala Ala Ala Thr
 325 330 335
 Gln Arg Leu Ala Asp Tyr Ser Pro Pro Ser Pro Ala Leu Ser Phe Ala
 340 345 350
 His Asn Gly Asn Asn Asn Asn Gly Asn Gly Tyr Thr Tyr Thr Ala
 355 360 365
 Gly Gly Glu Ala Ser Val Pro Ser Pro Asp Gly Cys Pro Glu Leu Gln
 370 375 380
 Pro Thr Phe Asp Pro Ala Pro Ala Pro Pro Gly Ala Pro Leu Ile
 385 390 395 400
 Trp Ala Gln Phe Glu Arg Ser Pro Gly Gly Pro Ala Ala Pro Val
 405 410 415
 Ser Ser Ser Cys Ser Ser Ser Ala Ser Ser Ser Ala Ser Ser Ser
 420 425 430
 Val Val Phe Pro Gly Gly Ala Ser Ala Pro Ser Asn Ala Asn Leu
 435 440 445
 Gly Leu Leu Val His Arg Arg Leu His Pro Gly Thr Ser Cys Pro Arg
 450 455 460
 Leu Ser Pro Pro Leu His Met Ala Pro Gly Ala Gly Glu His His Leu
 465 470 475 480
 Ala Arg Arg Val Arg Ser Asp Pro Gly Gly Gly Leu Ala Tyr Ala
 485 490 495
 Ala Tyr Ala Asn Gly Leu Gly Ala Gln Leu Pro Gly Leu Gln Pro Ser
 500 505 510
 Asp Thr Ser Gly Ser
 515 520 525
 Ser Ser Ser Ser Gly Leu Arg Arg Lys Gly Ser Arg Asp Cys Ser Val
 530 535 540
 Cys Phe Glu Ser Glu Val Ile Ala Ala Leu Val Pro Cys Gly His Asn
 545 550 555 560
 Leu Phe Cys Met Glu Cys Ala Asn Arg Ile Cys Glu Lys Ser Glu Pro
 565 570 575
 Glu Cys Pro Val Cys His Thr Ala Val Thr Gln Ala Ile Arg Ile Phe
 580 585 590
 Ser

<210> 73
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 73
 Met Pro Ser Ser Leu Phe Ala Asp Leu Glu Arg Asn Gly Ser Gly Gly
 1 5 10 15
 Gly Gly Gly Ser Ser Gly Gly Glu Thr Leu Asp Asp Gln Arg
 20 25 30
 Ala Leu Gln Leu Ala Leu Asp Gln Leu Ser Leu Leu Gly Leu Asp Ser
 35 40 45
 Asp Glu Gly Ala Ser Leu Tyr Asp Ser Glu Pro Arg Lys Lys Ser Val
 50 55 60
 Asn Met Thr Glu Cys Val Pro Val Pro Ser Ser Glu His Val Ala Glu
 65 70 75 80
 Ile Val Gly Arg Gln Gly Cys Lys Ile Lys Ala Leu Arg Ala Lys Thr
 85 90 95
 Asn Thr Tyr Ile Lys Thr Pro Val Arg Gly Glu Glu Pro Val Phe Val
 100 105 110
 Val Thr Gly Arg Lys Glu Asp Val Ala Met Ala Arg Arg Glu Ile Ile
 115 120 125

Ser Ala Ala Glu His Phe Ser Met Ile Arg Ala Ser Arg Asn Lys Asn
 130 135 140
 Thr Ala Leu Asn Gly Ala Val Pro Gly Pro Pro Asn Leu Pro Gly Gln
 145 150 155 160
 Thr Thr Ile Gln Val Arg Val Pro Tyr Arg Val Val Gly Leu Val Val
 165 170 175
 Gly Pro Lys Gly Ala Thr Ile Lys Arg Ile Gln Gln Gln Thr His Thr
 180 185 190
 Tyr Ile Val Thr Pro Ser Arg Asp Lys Glu Pro Val Phe Glu Val Thr
 195 200 205
 Gly Met Pro Glu Asn Val Asp Arg Ala Arg Glu Glu Ile Glu Ala His
 210 215 220
 Ile Ala Leu Arg Thr Gly Gly Ile Ile Glu Leu Thr Asp Glu Asn Asp
 225 230 235 240
 Phe His Ala Asn Gly Thr Asp Val Gly Phe Asp Leu His His Gly Ser
 245 250 255
 Gly Gly Ser Gly Pro Gly Ser Leu Trp Ser Lys Pro Thr Pro Ser Ile
 260 265 270
 Thr Pro Thr Pro Gly Arg Lys Pro Phe Ser Ser Tyr Arg Asn Asp Ser
 275 280 285
 Ser Ser Ser Leu Gly Ser Ala Ser Thr Asp Ser Tyr Phe Gly Gly Gly
 290 295 300
 Thr Ser Ser Ser Ala Ala Thr Gln Arg Leu Ala Asp Tyr Ser Pro
 305 310 315 320
 Ala Pro Ser Asn Ala Asn Leu Gly Leu Leu Val His Arg Arg Leu His
 325 330 335
 Pro Gly Thr Ser Cys Pro Arg Leu Ser Pro Pro Leu His Met Ala Pro
 340 345 350
 Gly Ala Gly Glu His His Leu Ala Arg Arg Val Arg Ser Asp Pro Gly
 355 360 365
 Gly Gly Gly Leu Ala Tyr Ala Ala Tyr Ala Asn Gly Leu Gly Ala Gln
 370 375 380
 Leu Pro Gly Leu Gln Pro Ser Asp Thr Ser Gly Ser Ser Ser Ser Ser
 385 390 395 400
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly Leu Arg Arg Lys
 405 410 415
 Gly Ser Arg Asp Cys Ser Val Cys Phe Glu Ser Glu Val Ile Ala Ala
 420 425 430
 Leu Val Pro Cys Gly His Asn Leu Phe Cys Met Glu Cys Ala Asn Arg
 435 440 445
 Ile Cys Glu Lys Ser Glu Pro Glu Cys Pro Val Cys His Thr Ala Val
 450 455 460
 Thr Gln Ala Ile Arg Ile Phe Ser
 465 470

<210> 74
 <211> 607
 <212> PRT
 <213> Homo sapiens

<400> 74

Met Trp Gly Leu Val Arg Leu Leu Ala Trp Leu Gly Gly Trp Gly
 1 5 10 15
 Cys Met Gly Arg Leu Ala Ala Pro Ala Arg Ala Trp Ala Gly Ser Arg
 20 25 30
 Glu His Pro Gly Pro Ala Leu Leu Arg Thr Arg Arg Ser Trp Val Trp
 35 40 45
 Asn Gln Phe Phe Val Ile Glu Glu Tyr Ala Gly Pro Glu Pro Val Leu
 50 55 60

Ile Gly Lys Leu His Ser Asp Val Asp Arg Gly Glu Gly Arg Thr Lys
 65 70 75 80
 Tyr Leu Leu Thr Gly Glu Gly Ala Gly Thr Val Phe Val Ile Asp Glu
 85 90 95
 Ala Thr Gly Asn Ile His Val Thr Lys Ser Leu Asp Arg Glu Glu Lys
 100 105 110
 Ala Gln Tyr Val Leu Leu Ala Gln Ala Val Asp Arg Ala Ser Asn Arg
 115 120 125
 Pro Leu Glu Pro Pro Ser Glu Phe Ile Ile Lys Val Gln Asp Ile Asn
 130 135 140
 Asp Asn Pro Pro Ile Phe Pro Leu Gly Pro Tyr His Ala Thr Val Pro
 145 150 155 160
 Glu Met Ser Asn Val Gly Thr Ser Val Ile Gln Val Thr Ala His Asp
 165 170 175
 Ala Asp Asp Pro Ser Tyr Gly Asn Ser Ala Lys Leu Val Tyr Thr Val
 180 185 190
 Leu Asp Gly Leu Pro Phe Ser Val Asp Pro Gln Thr Gly Val Val
 195 200 205
 Arg Thr Ala Ile Pro Asn Met Asp Arg Glu Thr Gln Glu Glu Phe Leu
 210 215 220
 Val Val Ile Gln Ala Lys Asp Met Gly Gly His Met Gly Gly Leu Ser
 225 230 235 240
 Gly Ser Thr Thr Val Thr Val Thr Leu Ser Asp Val Asn Asp Asn Pro
 245 250 255
 Pro Lys Phe Pro Gln Ser Leu Tyr Gln Phe Ser Val Val Glu Thr Ala
 260 265 270
 Gly Pro Gly Thr Leu Val Gly Arg Leu Arg Ala Gln Asp Pro Asp Leu
 275 280 285
 Gly Asp Asn Ala Leu Met Ala Tyr Ser Ile Leu Asp Gly Glu Gly Ser
 290 295 300
 Glu Ala Phe Ser Ile Ser Thr Asp Leu Gln Gly Arg Asp Gly Leu Leu
 305 310 315 320
 Thr Val Arg Lys Pro Leu Asp Phe Glu Ser Gln Arg Ser Tyr Ser Phe
 325 330 335
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 340 345 350
 Gly Pro Phe Lys Asp Val Ala Ser Val Arg Val Ala Val Gln Asp Ala
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 Pro Glu Pro Pro Ala Phe Thr Gln Ala Ala Tyr His Leu Thr Val Pro
 370 375 380
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 385 390 395 400
 Leu Asp Ser Pro Ala Ser Pro Ile Arg Tyr Ser Ile Leu Pro His Ser
 405 410 415
 Asp Pro Glu Arg Cys Phe Ser Ile Gln Pro Glu Glu Gly Thr Ile His
 420 425 430
 Thr Ala Ala Pro Leu Asp Arg Glu Ala Arg Ala Trp His Asn Leu Thr
 435 440 445
 Val Leu Ala Thr Glu Leu Val Pro Tyr Thr Pro Ala Tyr Ala Ser Gly
 450 455 460
 Ala Pro Pro Pro Phe Cys Leu His Thr Ala Tyr Glu Asn Cys Pro Cys
 465 470 475 480
 Ile Cys Gly Tyr Leu Asn Val Ser Val Lys Ala Tyr Met Asn Val His
 485 490 495
 Met Trp Ala Met Val Leu Val Phe Ala Glu His Lys Gly Gly Arg
 500 505 510
 Gly Pro Gly Arg Gln Ala Val Asp Gly Gln Lys Gln Ser Thr Arg Trp
 515 520 525
 Glu Leu Ser Gln Asn Cys Asn Tyr Leu Pro Lys Ser Arg Glu Gly Val

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Arg Gly Thr His Arg Asn Cys Thr Arg Ile Ala Cys His	Thr Arg Val	
565	570	575
Asn Pro Ile Leu Tyr His Ser Pro Thr Pro Gly His Arg	Thr Thr Tyr	
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Thr Cys Gly His Glu Tyr Ala Pro Ser Tyr Ala Glu Ser	Asn Thr	
595	600	605

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 <211> 781
 <212> PRT
 <213> Homo sapiens

<400> 75			
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Glu His Pro Gly Pro Ala Leu Leu Arg Thr Arg Arg Ser Trp Val Trp			
35	40	45	
Asn Gln Phe Phe Val Ile Glu Glu Tyr Ala Gly Pro Glu Pro Val Leu			
50	55	60	
Ile Gly Lys Leu His Ser Asp Val Asp Arg Gly Glu Gly Arg Thr Lys			
65	70	75	80
Tyr Leu Leu Thr Gly Glu Gly Ala Gly Thr Val Phe Val Ile Asp Glu			
85	90	95	
Ala Thr Gly Asn Ile His Val Thr Lys Ser Leu Asp Arg Glu Glu Lys			
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Pro Leu Glu Pro Pro Ser Glu Phe Ile Ile Lys Val Gln Asp Ile Asn			
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Asp Asn Pro Pro Ile Phe Pro Leu Gly Pro Tyr His Ala Thr Val Pro			
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Glu Met Ser Asn Val Gly Thr Ser Val Ile Gln Val Thr Ala His Asp			
165	170	175	
Ala Asp Asp Pro Ser Tyr Gly Asn Ser Ala Lys Leu Val Tyr Thr Val			
180	185	190	
Leu Asp Gly Leu Pro Phe Phe Ser Val Asp Pro Gln Thr Gly Val Val			
195	200	205	
Arg Thr Ala Ile Pro Asn Met Asp Arg Glu Thr Gln Glu Glu Phe Leu			
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Val Val Ile Gln Ala Lys Asp Met Gly Gly His Met Gly Gly Leu Ser			
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245	250	255	
Pro Lys Phe Pro Gln Ser Leu Tyr Gln Phe Ser Val Val Glu Thr Ala			
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Arg Val Glu Ala Thr Asn Thr Leu Ile Asp Pro Ala Tyr Leu Arg Arg			

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Glu Asn Lys Ala Pro Gly Thr Leu Val Gly Gln Ile Ser Ala Ala Asp		
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400		
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Asp Pro Glu Arg Cys Phe Ser Ile Gln Pro Glu Glu Gly Thr Ile His		
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Thr Ala Ala Pro Leu Asp Arg Glu Ala Arg Ala Trp His Asn Leu Thr		
435	440	445
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450	455	460
Val Ala Ile Gln Thr Leu Asp Glu Asn Asp Asn Ala Pro Gln Leu Ala		
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Glu Pro Tyr Asp Thr Phe Val Cys Asp Ser Ala Ala Pro Gly Gln Leu		
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Ile Gln Val Ile Arg Ala Leu Asp Arg Asp Glu Val Gly Asn Ser Ser		
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His Val Ser Phe Gln Gly Pro Leu Gly Pro Asp Ala Asn Phe Thr Val		
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Gln Asp Asn Arg Asp Gly Ser Ala Ser Leu Leu Leu Pro Ser Arg Pro		
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560		
Trp Gly Gln Pro Ala Leu Ser Ser Thr Ala Thr Val Thr Val Ser Val		
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Cys Arg Cys Gln Pro Asp Gly Ser Val Ala Ser Cys Trp Pro Glu Ala		
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His Leu Ser Ala Ala Gly Leu Ser Thr Gly Ala Leu Leu Ala Ile Ile		
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Thr Cys Val Gly Ala Leu Leu Ala Leu Val Val Leu Phe Val Ala Leu		
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640		
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Thr Glu Ala Phe Asp Ile Thr Ala Leu Gln Asn Pro Asp Gly Ala Ala		
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Leu Leu Ala Leu Arg Leu Arg Glu Ala Asp Glu Asp Pro Gly Val Pro		
705	710	715
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Pro Tyr Asp Ser Val Gln Val Tyr Gly Tyr Glu Gly Arg Gly Ser Ser		
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Cys Gly Ser Leu Ser Ser Leu Gly Ser Gly Ser Glu Ala Gly Gly Ala		
740	745	750
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 <211> 640
 <212> PRT

<213> Homo sapiens

<400> 76

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 35 40 45
 Ser Asp Pro Ser Gln Leu Asn Leu Tyr Met Arg Phe Glu Asp Glu Ser
 50 55 60
 Phe Asp Arg Leu Leu Trp Ser Ala Lys Glu Pro Ser Asp Ser Trp Leu
 65 70 75 80
 Ile Ala Ser Leu Asp Leu Gln Asn Ser Ser Lys Lys Phe Lys Ile Leu
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 Ile Glu Gly Val Leu Gly Gln Asn Thr Ala Ser Ile Ala Leu Phe
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 145 150 155 160
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 195 200 205
 Gln Gly Asn Asp Asn Val Phe Ser Leu Tyr Thr Arg Asp Val Ala Gly
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 Asn Leu Ala Glu Val Glu Phe Thr Cys His Phe Pro Leu Gln Val Ile
 245 250 255
 Phe Glu Val Ala Phe Asn Gly Pro Lys Gly Tyr Val Ala Leu Asp
 260 265 270
 Asp Ile Ser Phe Ser Pro Val His Cys Gln Asn Gln Thr Glu Leu Leu
 275 280 285
 Phe Ser Ala Val Glu Ala Ser Cys Asn Phe Glu Gln Asp Leu Cys Asn
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 Phe Tyr Gln Asp Lys Glu Gly Pro Gly Trp Thr Arg Val Lys Val Lys
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 Pro Asn Met Tyr Arg Ala Gly Asp His Thr Thr Gly Leu Gly Tyr Tyr
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 His Tyr Ala Ile Tyr Gly Phe Leu Lys Met Ser Asp Thr Leu Ala Val
 370 375 380
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 Lys Pro Met Pro Thr Lys Val Val Phe Met Ser Leu Cys Lys Ser Phe
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 Lys Ala Val Leu Leu Ser Pro Asp Leu Gln Ala Glu Glu Trp Ser Cys
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 Lys Met Thr Thr Gly Tyr Cys Ile Glu Cys Asp Phe Glu Glu Asn His
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 Gly Gly Gly Ser Ile Arg Asn Val His Ser Ile Leu Pro Gln Asp His
 195 200 205
 Thr Phe Lys Ser Glu Leu Gly His Tyr Met Tyr Val Asp Ser Val Tyr
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Val Lys His Phe Gln Glu Val Ala Gln Leu Ile Ser Pro Leu Thr Thr
 225 230 235 240
 Ala Pro Met Ala Gly Cys Leu Ser Phe Tyr Tyr Gln Ile Gln Gln Gly
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 Asn Asp Asn Val Phe Ser Leu Tyr Thr Arg Asp Val Ala Gly Leu Tyr
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 290 295 300
 Val Ala Phe Asn Gly Pro Lys Gly Gly Tyr Val Ala Leu Asp Asp Ile
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 Ser Phe Ser Pro Val His Cys Gln Asn Gln Thr Glu Leu Leu Phe Ser
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 370 375 380
 Ala Asn Thr Lys Phe Thr Ser Gln Pro Gly Tyr Ile Gly Arg Leu Tyr
 385 390 395 400
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 Cys Gly Leu Val Ala Leu Asp Asp Ile Thr Ile Gln Leu Gly Ser Cys
 485 490 495
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 Gln Asp Glu Cys Thr Phe Thr Gln Glu Lys Arg Asn Arg Ser Ser Trp
 515 520 525
 His Arg Arg Arg Gly Glu Thr Pro Thr Ser Tyr Thr Gly Pro Lys Gly
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 Asp His Thr Thr Gly Val Gly Tyr Tyr Met Tyr Ile Glu Ala Ser His
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 Met Val Tyr Gly Gln Lys Ala Arg Leu Leu Ser Arg Pro Leu Arg Gly
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 Glu Ala Ile Arg Gly Val Ser Ile Arg Ser Asp Ile Ala Ile Asp Asp
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<212> PRT
<213> Homo sapiens

<400> 78
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35 40 45
Glu Lys Leu Cys His Leu Gln Asp Cys Lys Val Asn Leu His Arg Ala
50 55 60
Ala Cys Gly Glu Cys Ile Val Ala Pro Lys Thr Ser Ser Phe Pro Tyr
65 70 75 80
Cys Gln Gly Thr Cys Leu Thr Leu Asn Ser Glu Leu His Gln Ser Asn
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Phe Ala Leu Lys Val Cys Thr Ile Arg Gly Glu Cys Leu Leu Ile Cys
100 105 110
Ser Trp Leu Phe Gln Thr Cys Ser Pro Thr Lys Val Ile Leu Phe Ser
115 120 125
Leu Thr Val Gln Asp Asp Glu Arg Lys Met Ser Val His Cys Val Asn
130 135 140
Ala Ser Leu Ile Glu Lys Cys Gly Cys Ser
145 150

INTERNATIONAL SEARCH REPORT

Inv — onal application No.
PCT/US01/13360

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) :C07H 21/04; C12P 21/06; C12N 9/00, 1/20, 15/00

US CL :435/69.1, 183, 252.2, 320.1; 536/23.2

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 183, 252.2, 320.1; 536/23.2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
BIOSIS, CAPLUS, MEDLINE, EMBASE, GENBANK, SCISEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, P	CARNINCI, P et al. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes, Genome Res., October 2000, Vol.10, No.10, pages 1617-1630, see entire article.	1-7
A, P	WO 00/55350 A1 (HUMAN GENOME SCIENCES, INC.) 21 September 2000 (21-9-00).	1-7
A	WO 95/30428 A1 (HUMAN GENOME SCIENCES, INC.) 16 November 1995 (11-16-95).	1-7
A	US 5,830,744 A (ROSEN et al.) 03 November 1998 (11-03-98).	1-7

Further documents are listed in the continuation of Box C.

See patent family annex.

•	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&"	document member of the same patent family
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

07 JULY 2001

Date of mailing of the international search report

02 AUG 2001

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-9230

Authorized Officer

MANJUNATH RAO

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/19360

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO:1 and 40

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US01/19960

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

- 1) Polynucleotide sequences with SEQ ID NOs 1 through 39.
- 2) Polypeptide sequences with SEQ ID NOs: 40-78.

The following claims are generic: Claims 1-7

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: Each of the above polynucleotide and polypeptide sequences are patentably distinct from each other as they have different structure and function.